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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:21:47 ; Search time 93.3333 Seconds
(without alignments)
38.435 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0
<Maximum DB seq length>: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	10	5	ABP53932 VEGFR-3 b
2	54	75.0	10	5	ABP53931 VEGFR-3 b
3	50	69.4	10	5	ABP53968 VEGFR-3 b
4	39.5	54.9	9	5	ABJ04472 Stem cell
5	35.5	49.3	9	5	ABJ04461 Stem cell
6	35	48.6	9	5	ABJ04460 Stem cell
7	33.5	46.5	7	5	ABJ04531 Molt-4 le
8	33	45.8	7	5	ABP53964 VEGFR-3 b
9	33	45.8	8	2	AAJ03715 Fluorine-
10	33	45.8	8	3	AAJ76817 Immunogen
11	33	45.8	8	5	ABP53965 VEGFR-3 b
12	33	45.8	8	7	ADG94005 Immunogen
13	33	45.8	8	8	ADL98014 Peptide h
14	33	45.8	10	5	ABB46346 Desmoglei
15	33	45.8	10	5	ABB46607 Desmocoll
16	32	44.4	7	3	AAJ76794 Somatosta
17	32	44.4	7	5	ABP53418 Backbone
18	32	44.4	9	4	ABP22609 HIV A11 m
19	32	44.4	9	4	ABP20314 HIV A03 m
20	32	44.4	9	5	AAU90543 Insulin/i
21	32	44.4	9	5	AAU90464 Insulin/i
22	32	44.4	9	5	AAU90542 Insulin/i
23	32	44.4	9	5	AAU90541 Insulin/i
24	32	44.4	10	2	AAW43886 Specific
25	32	44.4	10	3	AAJ66209 HLA-A3-bi

26	32	44.4	10	3	AAJ66213 HLA-A11-b
27	32	44.4	10	4	ABP20316 HIV A03 m
28	32	44.4	10	4	ABP20318 HIV A03 m
29	32	44.4	10	4	ABP22613 HIV A11 m
30	32	44.4	10	4	ABP14381 HIV A03 s
31	32	44.4	10	4	ABP22611 HIV A11 m
32	32	44.4	10	5	AAU88395 Insulin/i
33	32	44.4	10	5	AAU90462 Insulin/i
34	32	44.4	10	5	AAU90463 Insulin/i
35	32	44.4	10	5	AAU90535 Insulin/i
36	32	44.4	10	8	ADH58622 Radiophar
37	32	44.4	10	8	ADH58622 Radiophar
38	31	43.1	8	2	AAW97529 Antigenic
39	31	43.1	9	5	ABP53933 VEGFR-3 b
40	31	43.1	9	5	ABJ04488 HUVEC cel
41	31	43.1	9	8	ADN64476 HLA bindi
42	31	43.1	10	4	AAJ95260 Human com
43	30.5	42.4	10	2	AAJ14709 Labaditin
44	30	41.7	8	2	AAW12859 RGD-bind
45	30	41.7	8	3	AAJ91924 Residues

ALIGNMENTS

RESULT 1
ABP53932
ID ABP53932 standard; peptide; 10 AA.
XX
AC ABP53932;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:35.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.

XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 13; Page 80; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 72; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
| | | | | | | |
Db 1 CGYWLTIWGC 10

RESULT 2
ABP53931
ID ABP53931 standard; peptide; 10 AA.
XX
AC ABP53931;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:34.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnery; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "any amino acid"
FT Misc-difference 10 /note= "any amino acid"
FT
XX WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 12; Page 80; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 75.0%; Score 54; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
| | | | | | | |
Db 2 GYWLTIWG 9

RESULT 3
ABP53968
ID ABP53968 standard; peptide; 10 AA.
XX
AC ABP53968;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:73.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnery; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5. .7 /note= "X is any amino acid"
FT Misc-difference 9 /note= "X is any amino acid"
FT
XX WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Disclosure; Page 147; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a VEGFR-3 binding peptide, which is given in the
CC exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 69.4%; Score 50; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
Db 1 CGYWXXXWXC 10

RESULT 4
ABJ04472
ID ABJ04472 standard; peptide; 9 AA.
XX
AC ABJ04472;
XX
DT 24-OCT-2002 (first entry)
XX
DE Stem cell (mesenchymal) targeting peptide 61.
XX
KW BRASIL; targeting peptide; bacterial infection;
KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
KW viral infection; cardiovascular disease; degenerative disease.
XX
OS Unidentified.
XX
PN WO200220822-A2.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-US028124.
XX
PR 08-SEP-2000; 2000US-0231266P.
PR 17-JAN-2001; 2001US-00765101.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Arap W, Pasqualini R;
XX
DR WPI; 2002-404697/43.
XX
PT Identification of targeting peptides that can be used to treat diseases
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
PT of Selective Ligands) method comprises a single differential
PT centrifugation step.
XX
PS Example 5; Page 76; 167pp; English.
XX
CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
CC of Selective Interactive Ligands) to obtain a targeting peptide. The
CC BRASIL method of the invention involves: exposing a target to a phage
CC display library in a first phase; exposing the first phase to a second
CC phase; and separating the phage bound to the target from unbound phage.
CC The BRASIL method of the invention allows cell phages to be separated
CC from the remaining unbound phage in a single differential centrifugation
CC step. When compared to conventional cell panning methods, the BRASIL
CC method shows a significant increase in recovery of specific phage and a
CC substantial decrease in background. The BRASIL method is useful for
CC identifying targeting peptides. The targeting peptides identified by the
CC method of the invention are useful for treating disease states, such as:
CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
CC disease; bacterial infection; viral infection; cardiovascular disease and
CC degenerative disease. The present amino acid sequence represents a

CC targeting peptide of the invention
XX
SQ Sequence 9 AA;

Query Match 54.9%; Score 39.5; DB 5; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWLTIWGC 10
Db 1 CG-WFSWMGC 9

RESULT 5
ABJ04461
ID ABJ04461 standard; peptide; 9 AA.
XX
AC ABJ04461;
XX
DT 24-OCT-2002 (first entry)
XX
DE Stem cell (mesenchymal) targeting peptide 50.
XX
KW BRASIL; targeting peptide; bacterial infection;
KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
KW viral infection; cardiovascular disease; degenerative disease.
XX
OS Unidentified.
XX
PN WO200220822-A2.
XX
PD 14-MAR-2002.
XX
PF 07-SEP-2001; 2001WO-US028124.
XX
PR 08-SEP-2000; 2000US-0231266P.
PR 17-JAN-2001; 2001US-00765101.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Arap W, Pasqualini R;
XX
DR WPI; 2002-404697/43.
XX
PT Identification of targeting peptides that can be used to treat diseases
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
PT of Selective Ligands) method comprises a single differential
PT centrifugation step.
XX
PS Example 5; Page 76; 167pp; English.
XX
CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
CC of Selective Interactive Ligands) to obtain a targeting peptide. The
CC BRASIL method of the invention involves: exposing a target to a phage
CC display library in a first phase; exposing the first phase to a second
CC phase; and separating the phage bound to the target from unbound phage.
CC The BRASIL method of the invention allows cell phages to be separated
CC from the remaining unbound phage in a single differential centrifugation
CC step. When compared to conventional cell panning methods, the BRASIL
CC method shows a significant increase in recovery of specific phage and a
CC substantial decrease in background. The BRASIL method is useful for
CC identifying targeting peptides. The targeting peptides identified by the
CC method of the invention are useful for treating disease states, such as:
CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
CC disease; bacterial infection; viral infection; cardiovascular disease and
CC degenerative disease. The present amino acid sequence represents a
CC targeting peptide of the invention
XX
SQ Sequence 9 AA;

Query Match 49.3%; Score 35.5; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;.

Matches											5;	Conservative	2;	Mismatches	2;	Indels	1;	Gaps	1;	
QY	1 CGYWLTIWGC 10																			
	: :																			
Db	1 CGWW-GLWPC 9																			
RESULT 6																				
ABJ04460																				
ID	ABJ04460 standard; peptide; 9 AA.																			
XX	AC																			
	ABJ04460;																			
XX	24-OCT-2002 (first entry)																			
DT	Stem cell (mesenchymal) targeting peptide 49.																			
XX	BRASIL; targeting peptide; bacterial infection;																			
KW	Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;																			
KW	inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;																			
KW	viral infection; cardiovascular disease; degenerative disease.																			
XX	Unidentified.																			
OS	WO200220822-A2.																			
XX	14-MAR-2002.																			
PN	07-SEP-2001; 2001WO-US028124.																			
XX	08-SEP-2000; 2000US-0231266P.																			
PD	17-JAN-2001; 2001US-00765101.																			
XX	(TEXA) UNIV TEXAS SYSTEM.																			
PA	Arap W, Pasqualini R;																			
XX	WPI; 2002-404697/43.																			
PI	Identification of targeting peptides that can be used to treat diseases																			
XX	e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis																			
DR	of Selective Ligands) method comprises a single differential																			
XX	centrifugation step.																			
PT	Example 5; Page 76; 167pp; English.																			
PS	The invention comprises a method (BRASIL - Biopanning and Rapid Analysis																			
XX	of Selective Interactive Ligands) to obtain a targeting peptide. The																			
CC	BRASIL method of the invention involves: exposing a target to a phage																			
CC	display library in a first phase; exposing the first phase to a second																			
CC	phase; and separating the phage bound to the target from unbound phage.																			
CC	The BRASIL method of the invention allows cell phages to be separated																			
CC	from the remaining unbound phage in a single differential centrifugation																			
CC	step. When compared to conventional cell panning methods, the BRASIL																			
CC	method shows a significant increase in recovery of specific phage and a																			
CC	substantial decrease in background. The BRASIL method is useful for																			
CC	identifying targeting peptides. The targeting peptides identified by the																			
CC	method of the invention are useful for treating disease states, such as:																			
CC	diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune																			
CC	disease; bacterial infection; viral infection; cardiovascular disease and																			
CC	degenerative disease. The present amino acid sequence represents a																			
CC	targeting peptide of the invention																			
XX	Sequence 9 AA;																			
SQ	Query Match																			
	Best Local Similarity 48.6%; Score 35; DB 5; Length 9;																			
	Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;																			
QY	1 CGYWLTIW 8																			
	: :																			
Db	1 CDWWTTAW 8																			

RESULT 7	
ABJ04531	
ID	ABJ04531 standard; peptide; 7 AA.
XX	
AC	ABJ04531;
XX	
DT	24-OCT-2002 (first entry)
XX	
DE	Molt-4 leukaemia cell line targeting peptide 16.
XX	
KW	BRASIL; targeting peptide; bacterial infection;
KW	Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
KW	inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
KW	viral infection; cardiovascular disease; degenerative disease.
XX	
OS	Unidentified.
XX	
PN	WO200220822-A2.
XX	
PD	14-MAR-2002.
XX	
PF	07-SEP-2001; 2001WO-US028124.
XX	
PR	08-SEP-2000; 2000US-0231266P.
PR	17-JAN-2001; 2001US-00765101.
XX	
PA	(TEXA) UNIV TEXAS SYSTEM.
XX	
PI	Arap W, Pasqualini R;
XX	
DR	WPI; 2002-404697/43.
XX	
PT	Identification of targeting peptides that can be used to treat diseases
PT	e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
PT	of Selective Ligands) method comprises a single differential
PT	centrifugation step.
XX	
PS	Claim 79; Page 100; 167pp; English.
XX	
CC	The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
CC	of Selective Interactive Ligands) to obtain a targeting peptide. The
CC	BRASIL method of the invention involves: exposing a target to a phage
CC	display library in a first phase; exposing the first phase to a second
CC	phase; and separating the phage bound to the target from unbound phage.
CC	The BRASIL method of the invention allows cell phages to be separated
CC	from the remaining unbound phage in a single differential centrifugation
CC	step. When compared to conventional cell panning methods, the BRASIL
CC	method shows a significant increase in recovery of specific phage and a
CC	substantial decrease in background. The BRASIL method is useful for
CC	identifying targeting peptides. The targeting peptides identified by the
CC	method of the invention are useful for treating disease states, such as:
CC	diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
CC	disease; bacterial infection; viral infection; cardiovascular disease and
CC	degenerative disease. The present amino acid sequence represents a
CC	targeting peptide of the invention
XX	
SQ	Sequence 7 AA;
Query Match	46.5%; Score 33.5; DB 5; Length 7;
Best Local Similarity	50.0%; Pred. No. 1.7e+06;
Matches	5; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
QY	1 CGYWLTIWGC 10
Db	1 CSWV---WGC 7
RESULT 8	
ABP53964	
ID	ABP53964 standard; peptide; 7 AA.
XX	
AC	ABP53964;

XX 09-JAN-2003 (first entry)
DT
XX
DE VEGFR-3 binding peptide SEQ ID NO:67.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnery; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 4. .6
FT /note= "X is any amino acid"
XX
PN WO200257299-A2.
XX
PN
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PA Alitalo K, Koivunen E, Kubo H;
PI
XX WPI; 2002-691521/74.
DR
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 21; Page 81; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 7 AA;
Query Match 45.8%; Score 33; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GYWLTIW 8
| | | | |
Db 1 GYWXXXW 7
RESULT 9
AAY03715
ID AAY03715 standard; peptide; 8 AA.
XX
AC AAY03715;
XX
DT 08-JUN-1999 (first entry)

XX Fluorine-18 (F-18) labeled peptide 2.
DE
XX 18F radionuclide; targeting vector; positron emission tomography; F-18;
KW radiolabeling; thiol; fluorine-18.
KW
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "N-terminal acetylation; optionally has a free or
FT protected thiol group"
FT
FT Misc-difference 2 /note= "D-form residue"
FT
FT Misc-difference 3 /note= "D-form residue"
FT
FT Misc-difference 5 /note= "D-form residue; optionally has a free or
FT protected thiol group"
FT
FT Misc-difference 7 /note= "D-form residue"
FT
FT Misc-difference 8 /note= "D-form residue"
FT
XX WO9911590-A1.
PN
XX 11-MAR-1999.
PD
XX 03-SEP-1998; 98WO-US018268.
PF
XX 03-SEP-1997; 97US-0057485P.
PR
XX (IMMU-) IMMUNOMEDICS INC.
PA
XX Griffiths GL;
PI
XX WPI; 1999-228967/19.
DR
XX
PT Radiolabeling thiol-containing peptides with fluorine-18.
XX
PS Claim 14; Page 15; 22pp; English.
XX
CC The invention relates to a method for incorporating 18F radionuclide into
CC peptide-containing targeting vectors for use in clinical positron
CC emission tomography. Radiolabeling thiol-containing peptides with
CC fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol
CC group with a labeling reagent of formula: 18F-(CH2)m-CR1R2-(CH2)n-X, or a
CC fluorinated alkene in which at least one of the two double bonded carbon
CC atoms bears at least one leaving group comprising I, Br, Cl, azide,
CC tosylate, mesylate, nosylate or triflate. n, m = 0-2; n+m = 0-2; X = I,
CC Br, Cl, azide, tosylate, mesylate, nosylate, triflate, maleimide
CC (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I,
CC Br, Cl, azide, tosylate, mesylate, nosylate, triflate, H, CONH2, COOH,
CC OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl (optionally
CC substituted by CONH2, COOH, OH, sulfonic acid, tertiary amine or
CC quaternary ammonium), COOR', CONR'2 or COR'; and R' = 1-6C alkyl or
CC phenyl. The method is used for Radiolabeling peptide-containing targeting
CC vectors such as proteins, antibodies, antibody fragments and receptor-
CC targeted peptides for use in routine clinical positron emission
CC tomography. The method is simple and efficient. The method uses the
CC unique property of the free thiol groups which are rapidly alkylated at
CC neutral pH and moderate temperature. Sequences AAY03714-716 represent
CC examples of F-18 labeled peptides used in the method of detecting a
CC tissue
XX
SQ Sequence 8 AA;
Query Match 45.8%; Score 33; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGYW 4
| | | |

Db 5 CGYW 8

RESULT 10

AAAY76817

ID AAY76817 standard; peptide; 8 AA.

XX

AC AAY76817;

XX

DT 28-APR-2000 (first entry)

XX

DE Immunogenic peptide for bi-specific antibody recognition.

XX

KW Immunogenic peptide; bi-specific antibody; diagnosis; immune response;

KW diseased tissue identification; therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1 /note= "acetylated; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"

FT

FT Misc-difference 2 /note= "D-form residue"

FT

FT Misc-difference 3 /note= "D-form residue"

FT

FT Misc-difference 5 /note= "D-form residue"

FT

FT /note= "D-form residue; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"

FT

FT Misc-difference 7 /note= "D-form residue"

FT

FT Misc-difference 8 /note= "D-form residue"

FT

XX WO9966951-A2.

PN

XX

PD 29-DEC-1999.

XX

XX

PF 22-JUN-1999; 99WO-US013879.

XX

PR 22-JUN-1998; 98US-0090142P.

PR

PR 14-OCT-1998; 98US-0104156P.

XX

PA (IMMU-) IMMUNOMEDICS INC.

XX

PI Hansen HJ, Griffiths GL, Leung S, McBride WJ, Qu Z;

XX

XX WPI; 2000-160561/14.

DR

XX

PT Bi-specific antibodies that bind specific target tissue and targeted conjugates.

PT

XX

PS Claim 22; Page 61; 76pp; English.

XX

CC This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method

XX

SQ Sequence 8 AA;

Query Match 45.8%; Score 33; DB 3; Length 8;

Best Local Similarity 100.0%; Pred.No. 1.7e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYW 4

Db 5 CGYW 8

RESULT 11

ABP53965

ID ABP53965 standard; peptide; 8 AA.

XX

AC ABP53965;

XX

DT 09-JAN-2003 (first entry)

XX

DE VEGFR-3 binding peptide SEQ ID NO:68.

XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnery; cell surface receptor; cancer; neovascularisation; liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 4. .6 /note= "X is any amino acid"

FT

FT Misc-difference 8 /note= "any amino acid"

FT

XX WO200257299-A2.

PN

XX

PD 25-JUL-2002.

XX

PF 16-JAN-2002; 2002WO-IB0000099.

XX

PR 17-JAN-2001; 2001US-0262476P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA LTD.

XX

PI Alitalo K, Koivunen E, Kubo H;

XX

XX WPI; 2002-691521/74.

DR

XX

PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

PT

XX

PS Claim 22; Page 81; 149pp; English.

XX

CC The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnery activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention

XX

SQ Sequence 8 AA;

Query Match 45.8%; Score 33; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 1 GYWXXXW 7

RESULT 12
ADG94005
ID ADG94005 standard; peptide; 8 AA.
XX AC ADG94005;
XX DT 11-MAR-2004 (first entry)
XX AC Immunogenic peptide.
DE DE Immunogenic peptide; multi-specific antibody; polymer conjugate; tumour;
KW KW cytostatic; photodynamic therapy.
KW OS Synthetic.
XX FH Key Location/Qualifiers
FT FT Modified-site 1 /note= "Optionally methylated or Acetylated"
FT FT Misc-difference 2 /note= "D-form residue"
FT FT Misc-difference 3 /note= "D-form residue"
FT FT Misc-difference 5 /note= "optionally methylated or Acetylated D-form residue"
FT FT Misc-difference 7 /note= "D-form residue"
FT FT Misc-difference 8 /note= "D-form residue"
FT FT US2003026764-A1.
XX PD 06-FEB-2003.
XX PF 31-JUL-2002; 2002US-00209592.
XX PR 31-JUL-2001; 2001US-0308605P.
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Griffiths GL;
XX DR WPI; 2003-801085/75.
XX Targeting an agent towards a target site in a tissue, by administering in a tissue, a multi-specific antibody or its fragment and a polymer conjugate that binds to the capture arm of the multi-specific antibody.
PS Disclosure; Page 14; 19pp; English.
XX The invention relates to targeting an agent towards a target site in a tissue, comprising administering to the tissue, a multi-specific antibody or its fragment, comprising a targeting arm that binds to an antigen of the target site and a capture arm that binds to a polymer conjugate, and administering a polymer conjugate that binds to the capture arm, the conjugate has a polymer conjugated to the agent such as therapeutic agent, a peptide, an enzyme and a labelled ligand. Also included is a kit useful for targeting a target site within a tissue in a subject or tissue sample comprising the above mentioned multi-specific antibody or its fragment and a polymer conjugate. The method is used for targeting an agent towards a target site in a tissue (e.g. a tumour). The method is also useful for therapeutic or diagnostic purposes and further in photodynamic therapy. The present sequence is an immunogenic peptide used

CC in the method of the invention.
XX SQ Sequence 8 AA;
Query Match 45.8%; Score 33; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGYW 4
Db 5 CGYW 8

RESULT 13
ADL98014
ID ADL98014 standard; peptide; 8 AA.
XX AC ADL98014;
XX DT 20-MAY-2004 (first entry)
DE DE Peptide hapten #2.
XX KW photodynamic diagnosis; cancer; tumour; cardiovascular lesion;
KW KW inflammatory disease; neurodegenerative disease; metabolic disease;
KW KW infectious disease; B-cell malignancy; Alzheimer's disease; amyloidosis;
KW KW autoimmune disease; bacterial infection; fungal infection;
KW KW parasitic infection; viral infection;
KW KW carcinoembryonic antigen-expressing tumour.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT FT Modified-site 1 /note= "Optionally Cysteiny1; if Cys the residue is methylated; N-terminal acetylated."
FT FT Misc-difference 2 /note= "D form residue"
FT FT Misc-difference 3 /note= "D form residue"
FT FT Modified-site 5 /note= "Optionally Cysteiny1; if Cys the residue is methylated; N-terminal acetylated."
FT FT Misc-difference 7 /note= "D form residue"
FT FT Misc-difference 8 /note= "D form residue"
XX PN US2004043030-A1.
XX PD 04-MAR-2004.
XX PF 09-JUN-2003; 2003US-00456580.
XX PR 31-JUL-2001; 2001US-0308605P.
XX PR 31-JUL-2002; 2002US-00209592.
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Griffiths GL, Goldenberg DM, Hansen HJ;
XX DR WPI; 2004-313738/29.
XX Treating cancer and metabolic diseases by administering a multi-specific antibody having a targeting arm that binds to an antigen and a capture arm that binds to a polymer conjugate comprising a therapeutic agent.
PS Disclosure; Page 16; 24pp; English.
XX The invention relates to a method of diagnosing or treating a disease or disorder. The method involves administering to a tissue a multi-specific antibody (I) or antibody fragment, comprising a targeting arm that binds to an antigen on the target site, and a capture arm that binds to a

CC polymer conjugate, and administering to the tissue a polymer conjugate
CC that binds to the capture arm, the polymer conjugate comprising a polymer
CC conjugated to a diagnostic or therapeutic agent. Also included is a
CC method for photodynamic diagnosis or treatment of a disease or disorder,
CC or intravascular or endoscopic method for diagnosing or treating a
CC disease or disorder. The method is useful for diagnosing or treating a
CC disease or disorder chosen from cancer (oesophageal, gastric, colonic,
CC rectal, pancreatic, lung, breast, ovarian, urinary bladder, endometrial,
CC cervical, testicular, renal, adrenal and liver cancer, solid tumour, B-
CC cell malignancy or T-cell malignancy); cardiovascular lesion; an
CC inflammatory disease; neurodegenerative disease; metabolic disease; and
CC an infectious disease. The B-cell malignancy is chosen from indolent
CC forms of B-cell lymphomas, aggressive forms of B-cell lymphomas, chronic
CC lymphatic leukaemias, acute lymphatic leukaemias, and multiple myeloma.
CC The solid tumour is chosen melanoma, carcinoma (preferably renal
CC carcinoma, lung carcinoma, intestinal carcinoma, and stomach carcinoma),
CC glioma and sarcoma. The cardiovascular lesion is chosen from infarct,
CC clot, embolus, atherosclerotic plaque and ischaemia. The
CC neurodegenerative disease is Alzheimer's disease. The metabolic disease
CC is amyloidosis, where the antibody binds amyloid. The disease or disorder
CC is displaced or ectopic normal tissue chosen from endometrium, thymus,
CC spleen and parathyroid. The method can be used for normal tissue
CC ablation, where the tissue is chosen from bone marrow and spleen. The
CC disease or disorder is an autoimmune disease such as myasthenia gravis,
CC lupus nephritis, lupus erythematosus, and rheumatoid arthritis, Class III
CC autoimmune diseases such as immune-mediated thrombocytopenias, such as
CC acute idiopathic thrombocytopenic purpura and chronic idiopathic
CC thrombocytopenic purpura, dermatomyositis, Sjogren's syndrome, multiple
CC sclerosis, Sydenham's chorea, myasthenia gravis, systemic lupus
CC erythematosus, lupus nephritis, rheumatic fever, polyglandular syndromes,
CC bullous pemphigoid, diabetes mellitus, Henoch-Schonlein purpura, post-
CC streptococcal nephritis, erythema nodosum, Takayasu's arteritis,
CC Addison's disease, rheumatoid arthritis, sarcoidosis, ulcerative colitis,
CC erythema multiforme, IGA nephropathy, polyarteritis nodosa, ankylosing
CC spondylitis, Goodpasture's syndrome, thromboangitis obliterans, primary
CC biliary cirrhosis, Hashimoto's thyroiditis, thyrotoxicosis, scleroderma,
CC chronic active hepatitis, polymyositis/dermatomyositis, polychondritis,
CC pemphigus vulgaris, Wegener's granulomatosis, membranous nephropathy,
CC amyotrophic lateral sclerosis, tabes dorsalis, giant cell
CC arteritis/polymyalgia, pernicious anaemia, rapidly progressive
CC glomerulonephritis, or fibrosing alveolitis. The infectious disease is
CC chosen from bacterial, fungal, parasitic and viral lesion. The infectious
CC disease is caused by a fungus chosen from Microsporium, Trichophyton,
CC Epidermophyton, Sporothrix schenckii, Cyrtococcus neoformans,
CC Coccidioides immitis, Histoplasma capsulatum, Blastomyces dermatitidis,
CC and Candida albicans. The infectious disease is caused by a virus chosen
CC from HIV, herpes virus, cytomegalovirus, rabies virus, influenza virus,
CC hepatitis B virus, Sendai virus, feline leukemia virus, Reo virus, polio
CC virus, human serum parvo-like virus, simian virus 40, respiratory
CC syncytial virus, mouse mammary tumour virus, Varicella-Zoster virus,
CC Dengue virus, rubella virus, measles virus, adenovirus, human T-cell
CC leukemia viruses, Epstein-Barr virus, murine leukemia virus, mumps virus,
CC vesicular stomatitis virus, Sindbis virus, lymphocytic choriomeningitis
CC virus, wart virus and blue tongue virus. The infectious disease is caused
CC by a bacterium chosen from Bacillus anthracis, Streptococcus agalactiae,
CC Legionella pneumophila, Streptococcus pyogenes, Escherichia coli,
CC Neisseria gonorrhoeae, Neisseria meningitidis, Pneumococcus, Haemophilus
CC influenzae B, Treponema pallidum, Lyme disease spirochetes, Pseudomonas
CC aeruginosa, Mycobacterium leprae , Brucella abortus , Mycobacterium
CC tuberculosis , and Tetanus toxin . The infectious disease is caused by a
CC protozoa chosen from Plasmodium falciparum, Plasmodium vivax, Toxoplasma
CC gondii, Trypanosoma rangeli , Trypanosoma cruzi, Trypanosoma
CC rhodesiensei, Trypanosoma brucei, Schistosoma mansoni, Schistosoma
CC japonicum, Babesia bovis, Elmeria tenella, Onchocerca volvulus, Theileria
CC Leishmania tropica, Trichinella spiralis, Onchocerca volvulus, Echinococcus
CC parva, Taenia hydatigena, Taenia ovis, Taenia saginata, Echinococcus
CC granulosis, and Mesocostoides corti. The infectious disease is caused by
CC a mycoplasma chosen from Mycoplasma arthritidis, M. hyorhinis, M. orale,
CC M. arginini, Acholeplasma laidlawii, M. salivarium and M. pneumoniae. The
CC cancer is preferably chosen from carcinoembryonic antigen (CEA) -
CC expressing tumour or a CD20-expressing malignancy. The present sequence
CC represents a peptide used in the method of the invention.

SQ Sequence 8 AA;
Query Match 45.8%; Score 33; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGYW 4
Db 5 CGYW 8
RESULT 14
ABB46346
ID ABB46346 standard; peptide; 10 AA.
XX
AC ABB46346;
XX
DT 30-JAN-2002 (first entry)
XX
DE Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.
XX
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytotostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
XX
OS Synthetic.
XX
PN WO200172956-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-IB001400.
XX
PR 27-MAR-2000; 2000US-00535852.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Symonds JM, Gour BJ;
XX
XX WPI; 2002-025778/03.
DR
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
PS Claim 18; Page 101; 127pp; English.
XX
CC The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer (e.g.
CC carcinoma, leukaemia or melanoma) and induce apoptosis
XX
SQ Sequence 10 AA;
Query Match 45.8%; Score 33; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGYWLTIWGC 10
Db 1 CGYALDARGC 10
RESULT 15

ABB46607
ID ABB46607 standard; peptide; 10 AA.
XX
AC ABB46607;
XX
DT 30-JAN-2002 (first entry)
XX
DE Desmocollin-1 CAR cyclic peptide 9.
XX
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytosolic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
XX
OS Synthetic.
XX
PN WO200172956-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-IB001400.
XX
PR 27-MAR-2000; 2000US-00535852.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Symonds JM, Gour BJ;
XX
DR WPI; 2002-025778/03.
XX
PT Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
PS Claim 23; Page 109; 127pp; English.
XX
CC The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer (e.g.
CC carcinoma, leukaemia or melanoma) and induce apoptosis
XX
SQ Sequence 10 AA;

Query Match 45.8%; Score 33; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
||| |
Db 1 CGYATTADGC 10

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OM protein - protein search, using sw model

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(without alignments)
28.022 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 110780

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Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	33	45.8	10	4	US-09-535-852-1090
2	33	45.8	10	4	US-09-535-852-1090
3	30	41.7	8	2	US-08-520-535-12
4	30	41.7	8	2	US-09-079-432-12
5	30	41.7	9	2	US-08-986-234-92
6	30	41.7	9	4	US-09-311-784A-374
7	30	41.7	9	4	US-09-790-497A-1
8	30	41.7	10	3	US-09-108-709-22
9	30	41.7	10	4	US-09-790-497A-110
10	29	40.3	5	1	US-07-946-237-4
11	29	40.3	5	2	US-08-530-566-10
12	29	40.3	5	3	US-09-195-726-10
13	29	40.3	5	3	US-09-067-755-10
14	29	40.3	5	4	US-08-239-765C-4
15	29	40.3	7	4	US-09-069-827A-94
16	29	40.3	9	4	US-09-311-784A-348
17	29	40.3	10	2	US-08-735-253-8
18	29	40.3	10	2	US-08-735-253-13
19	29	40.3	10	3	US-08-481-968A-21
20	29	40.3	10	3	US-08-154-712B-21
21	29	40.3	10	4	US-09-947-925A-21
22	28	38.9	8	3	US-09-315-304B-1649
23	28	38.9	10	1	US-08-250-789A-119
24	28	38.9	10	4	US-09-462-917A-73
25	28	38.9	10	4	US-09-125-641-3
26	28	38.9	10	4	US-09-790-497A-5
27	28	38.9	10	4	US-09-790-497A-24

28	27.5	38.2	6	1	US-08-191-571-12	Sequence 12, Appl
29	27.5	38.2	6	5	PCT-US95-00296-12	Sequence 12, Appl
30	27	37.5	8	3	US-08-925-002-12	Sequence 12, Appl
31	27	37.5	8	3	US-08-586-670A-17	Sequence 17, Appl
32	27	37.5	8	3	US-09-082-279B-1495	Sequence 1495, Ap
33	27	37.5	8	4	US-09-834-784-1495	Sequence 1495, Ap
34	27	37.5	8	4	US-09-910-552-12	Sequence 12, Appl
35	27	37.5	8	4	US-09-350-641C-1650	Sequence 1650, Ap
36	27	37.5	10	3	US-09-315-304B-1587	Sequence 1587, Ap
37	27	37.5	10	4	US-09-350-325-47	Sequence 47, Appl
38	27	37.5	10	4	US-09-535-852-1357	Sequence 1357, Ap
39	27	37.5	10	4	US-09-350-641C-1587	Sequence 1587, Ap
40	27	37.5	10	4	US-09-239-043D-2474	Sequence 2474, Ap
41	27	37.5	10	4	US-09-620-091-28	Sequence 28, Appl
42	27	37.5	10	4	US-09-620-091-42	Sequence 42, Appl
43	27	37.5	10	4	US-09-620-091-47	Sequence 47, Appl
44	26.5	36.8	10	3	US-09-186-958-12	Sequence 12, Appl
45	26.5	36.8	10	3	US-09-669-271A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-535-852-1090
; Sequence 1090, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-09-535-852-1090

Query Match 45.8%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
||| |
Db 1 CGYALDARGC 10

RESULT 2
US-09-535-852-1352
; Sequence 1352, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1352
; LENGTH: 10

```
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1352

Query Match          45.8%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
      .| | | |
Db      1 CGYATTADGC 10

RESULT 3
US-08-520-535-12
; Sequence 12, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-520-535-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWL 5
      .| | | |
Db      1 CDYWL 5

RESULT 4
US-09-079-432-12
; Sequence 12, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,432
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/520,535
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-079-432-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWL 5
      .| | | |
Db      1 CDYWL 5

RESULT 5
US-08-986-234-92
; Sequence 92, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-986-234-92

Query Match          41.7%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 IWGC 10
      .| | | |
Db      2 IWGC 5

RESULT 6
US-09-311-784A-374
; Sequence 374, Application US/09311784A
; Patent No. 6534482
```


; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)
US-09-311-784A-374

Query Match 41.7%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
Db 1 IWGC 4

RESULT 7
US-09-790-497A-1
; Sequence 1, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-790-497A-1

Query Match 41.7%; Score 30; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
Db 1 IWGC 4

Db 1 IWGC 4

RESULT 8
US-09-108-709-22
; Sequence 22, Application US/09108709
; Patent No. 6008044
; GENERAL INFORMATION:
; APPLICANT: Cotropia, Joseph P.
; TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane G
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis T-
; TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibiting
; TITLE OF INVENTION: Fusion-associated Epitope (GCSGKLIC) in gp-41
; FILE REFERENCE: 10586/00406
; CURRENT APPLICATION NUMBER: US/09/108,709
; CURRENT FILING DATE: 1998-07-01
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: amino acids 600-609 according to the Gnann
; OTHER INFORMATION: numbering system
US-09-108-709-22

Query Match 41.7%; Score 30; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
Db 1 IWGC 4

RESULT 9
US-09-790-497A-110
; Sequence 110, Application US/09790497A
; Patent No. 6649735
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-16
; CURRENT APPLICATION NUMBER: US/09/790,497A
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/576,824
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-790-497A-110

Query Match 41.7%; Score 30; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 IWGC 10
|||
Db 1 IWGC 4

RESULT 10
US-07-946-237-4
; Sequence 4, Application US/07946237
; Patent No. 5348874
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,237
; FILING DATE: 19920914
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: David E. Brook
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BTT92-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: AMINO ACID
; MOLECULE TYPE: peptide
US-07-946-237-4

Query Match 40.3%; Score 29; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
:|
Db 2 VWGC 5

RESULT 11
US-08-530-566-10
; Sequence 10, Application US/08530566
; Patent No. 5840865
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,566
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,765
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,237
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: BTT92-01ZA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-530-566-10

Query Match 40.3%; Score 29; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
:|
Db 2 VWGC 5

RESULT 12
US-09-195-726-10
; Sequence 10, Application US/09195726
; Patent No. 6159717
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/195,726
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/530,566
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,765
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/946,237
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Alice O.
; REGISTRATION NUMBER: 33,542
; REFERENCE/DOCKET NUMBER: IMBB92-01ZAZ
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-195-726-10

Query Match 40.3%; Score 29; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
:||||
Db 2 VWGC 5

RESULT 13

US-09-067-755-10
; Sequence 10, Application US/09067755
; Patent No. 6225121
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; APPLICANT: Klinakis, Apostolos G.
; TITLE OF INVENTION: Eukaryotic Transposable Element
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,755
; FILING DATE: 27-APR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/530,566
; FILING DATE: 20-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/239,765
; FILING DATE: 09-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,237
; FILING DATE: 14-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Alice O.
; REGISTRATION NUMBER: 33,542
; REFERENCE/DOCKET NUMBER: IMBB92-01ZAZ
; TELEPHONE: (781) 861-6240
; TELEFAX: (781) 861-9540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-067-755-10

Query Match 40.3%; Score 29; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
:||||
Db 2 VWGC 5

RESULT 14

US-08-239-765C-4
; Sequence 4, Application US/08239765C
; Patent No. 6469228
; GENERAL INFORMATION:
; APPLICANT: Savakis, Charalambos
; APPLICANT: Franz, Gerald H.
; APPLICANT: Loukeris, Athanasios
; TITLE OF INVENTION: Eukaryotic Transposable Element
; FILE REFERENCE: 18747/1130
; CURRENT APPLICATION NUMBER: US/08/239,765C
; CURRENT FILING DATE: 1994-05-09
; PRIOR APPLICATION NUMBER: 07/946,237
; PRIOR FILING DATE: 1992-09-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Conserved amino acid sequence of the TC-1 family of transposable
; OTHER INFORMATION: elements
US-08-239-765C-4

Query Match 40.3%; Score 29; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
:||||
Db 2 VWGC 5

RESULT 15

US-09-069-827A-94
; Sequence 94, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M
; KAY, Brian K
; FRELINGER, Jeffrey A
; HYDE-DERUYSCHE, Robin P
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
; COMPLEMENTARY COMBINATORIAL LIBRARIES
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES-4C
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
;
; INFORMATION FOR SEQ ID NO: 94:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
;
; US-09-069-827A-94

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Query Match	40.3%	Score 29;	DB 4;	Length 7;
Best Local Similarity	57.1%	Pred. No. 3.8e+05;		
Matches 4;	Conservative	0;	Mismatches 3;	Indels 0;
Gaps	0;			

QY 3 YWLTWG 9
|||
Db 1 YWVPDWG 7

Search completed: December 30, 2004, 14:44:16
Job time : 24.6667 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:43:15 ; Search time 81.3333 Seconds
(without alignments)
44.229 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 182644

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	72	100.0	10	13	US-10-046-922-35	Sequence 35, Appl
2	54	75.0	10	13	US-10-046-922-34	Sequence 34, Appl
3	50	69.4	10	13	US-10-046-922-73	Sequence 73, Appl
4	33	45.8	7	13	US-10-046-922-67	Sequence 67, Appl
5	33	45.8	8	13	US-10-046-922-68	Sequence 68, Appl
6	33	45.8	10	17	US-10-046-922-1090	Sequence 1090, Ap
7	33	45.8	10	17	US-10-654-578-1090	Sequence 1352, Ap
8	32	44.4	10	8	US-08-821-739A-90	Sequence 90, Appl
9	32	44.4	10	14	US-10-133-210-39	Sequence 39, Appl
10	32	44.4	10	14	US-10-133-210-69	Sequence 69, Appl
11	31	43.1	9	13	US-10-046-922-36	Sequence 36, Appl
12	31	43.1	10	10	US-09-572-404B-1454	Sequence 1454, Ap
13	30	41.7	9	8	US-08-821-739A-78	Sequence 78, Appl

14	30	41.7	9	9	US-09-832-723-104	Sequence 104, App
15	30	41.7	9	9	US-09-894-018-80	Sequence 80, Appl
16	30	41.7	9	9	US-09-894-018-185	Sequence 185, App
17	30	41.7	9	14	US-10-303-331-104	Sequence 104, App
18	30	41.7	9	14	US-10-371-525-374	Sequence 374, App
19	30	41.7	9	14	US-10-371-069-374	Sequence 374, App
20	30	41.7	9	14	US-10-371-645-374	Sequence 374, App
21	30	41.7	9	14	US-10-371-260-374	Sequence 374, App
22	30	41.7	9	17	US-10-474-960A-80	Sequence 80, Appl
23	30	41.7	9	17	US-10-474-960A-185	Sequence 185, App
24	30	41.7	10	15	US-10-462-452-707	Sequence 707, App
25	30	41.7	10	15	US-10-601-953-812	Sequence 812, App
26	30	41.7	10	16	US-10-322-266-708	Sequence 708, App
27	29	40.3	5	8	US-08-239-765B-4	Sequence 4, Appli
28	29	40.3	9	9	US-09-894-018-154	Sequence 154, App
29	29	40.3	9	14	US-10-133-210-8	Sequence 8, Appli
30	29	40.3	9	14	US-10-371-525-348	Sequence 348, App
31	29	40.3	9	14	US-10-371-069-348	Sequence 348, App
32	29	40.3	9	14	US-10-371-645-348	Sequence 348, App
33	29	40.3	9	14	US-10-371-260-348	Sequence 348, App
34	29	40.3	9	15	US-10-182-252A-180	Sequence 180, App
35	29	40.3	9	15	US-10-182-252A-181	Sequence 181, App
36	29	40.3	9	15	US-10-182-252A-305	Sequence 305, App
37	29	40.3	9	15	US-10-182-252A-792	Sequence 792, App
38	29	40.3	9	15	US-10-182-252A-793	Sequence 793, App
39	29	40.3	9	15	US-10-182-252A-837	Sequence 837, App
40	29	40.3	9	15	US-10-182-252A-838	Sequence 838, App
41	29	40.3	9	15	US-10-182-252A-1271	Sequence 1271, Ap
42	29	40.3	9	17	US-10-474-960A-154	Sequence 154, App
43	29	40.3	10	8	US-08-821-739A-92	Sequence 92, Appl
44	29	40.3	10	9	US-09-947-925A-21	Sequence 21, Appl
45	29	40.3	10	14	US-10-094-401-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match 100.0%; Score 72; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
| | | | | | | | | |
Db 1 CGYWLTIWGC 10

RESULT 2
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki

; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 75.0%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
Db 2 GYWLTIWG 9

RESULT 3
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide library
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(7)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-73

Query Match 69.4%; Score 50; DB 13; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10
Db 1 CGYWXXXWXC 10

RESULT 4
US-10-046-922-67
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime

; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-046-922-67

Query Match 45.8%; Score 33; DB 13; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
Db 1 GYWXXXW 7

RESULT 5
US-10-046-922-68
; Sequence 68, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68

Query Match 45.8%; Score 33; DB 13; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
Db 1 GYWXXXW 7

RESULT 6
US-10-654-578-1090
; Sequence 1090, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578

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; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1090
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence
US-10-654-578-1090

Query Match          45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
      |||||
Db      1 CGYALDARGC 10

RESULT 7
US-10-654-578-1352
; Sequence 1352, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1352
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1352

Query Match          45.8%; Score 33; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGYWLTIWGC 10
      |||||
Db      1 CGYATTADGC 10

RESULT 8
US-08-821-739A-90
; Sequence 90, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; PRIOR FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
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; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-90

Query Match          44.4%; Score 32; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LTIWGC 10
      |||||
Db      2 LGIWGC 7

RESULT 9
US-10-133-210-39
; Sequence 39, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-39

Query Match          44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LTIWGC 10
      |||||
Db      2 LGIWGC 7

RESULT 10
US-10-133-210-69
; Sequence 69, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: DeLisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
```

; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-69

Query Match 44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 LTIWGC 10
| | | | |
Db 2 LGIWGC 7

RESULT 11
US-10-046-922-36
; Sequence 36, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-36

Query Match 43.1%; Score 31; DB 13; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
| | | | |
Db 2 GYWWDTW 8

RESULT 12
US-09-572-404B-1454
; Sequence 1454, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1454
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in p2RY5 at 139-148 and may interact with Sequen

; OTHER INFORMATION: in this patent.
US-09-572-404B-1454

Query Match 43.1%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9
| | | | |
Db 1 GVWLTVIG 8

RESULT 13
US-08-821-739A-78
; Sequence 78, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-78

Query Match 41.7%; Score 30; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
| | | | |
Db 1 IWGC 4

RESULT 14
US-09-832-723-104
; Sequence 104, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-104

Query Match 41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIW 8
| | | | |
Db 1 CTLWPTEW 8

RESULT 15
US-09-894-018-80
; Sequence 80, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-09-894-018-80

Query Match 41.7%; Score 30; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
| | | | |
Db 1 IWGC 4

Search completed: December 30, 2004, 15:04:06
Job time : 81.3333 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:30:43 ; Search time 18.6667 Seconds
(without alignments)
51.545 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	33.3	10	2 S71868	glutathione transf
2	24	33.3	10	2 A35556	hypothetical prote
3	22	30.6	7	2 PT0586	T-cell receptor be
4	22	30.6	10	2 T17075	cytochrome-c oxida
5	21	29.2	10	2 E41946	T-cell receptor ga
6	20	27.8	5	2 JH0253	gut pentapeptide -
7	20	27.8	6	2 F41946	T-cell receptor ga
8	20	27.8	8	2 S19288	acylase - Kluyvera
9	19	26.4	9	2 PT0324	Ig heavy chain CRD
10	19	26.4	10	2 PT0289	Ig heavy chain CRD
11	19	26.4	10	2 E49033	T-cell receptor ga
12	19	26.4	10	2 F49033	T-cell receptor ga
13	19	26.4	10	2 C41946	leucokinin V - Mad
14	18	25.0	8	2 JS0315	Ig heavy chain CDR
15	18	25.0	10	2 PT0230	T-cell receptor be
16	18	25.0	10	2 PH0923	Ig mu chain J regi
17	18	25.0	10	2 F33932	UGA3 leader peptid
18	18	25.0	10	4 S14943	T-cell receptor be
19	17	23.6	4	2 B53284	T-cell receptor be
20	17	23.6	6	2 PT0629	T-cell receptor be
21	17	23.6	6	2 PT0637	T-cell receptor be
22	17	23.6	6	2 A61068	locustakinin - mig
23	17	23.6	6	4 I79564	hypothetical TCL3
24	17	23.6	7	2 PT0628	T-cell receptor be
25	17	23.6	7	2 PT0642	T-cell receptor be
26	17	23.6	7	2 PT0722	T-cell receptor be
27	17	23.6	7	2 PT0728	T-cell receptor be
28	17	23.6	7	2 PX0008	glucuronosyltransf
29	17	23.6	7	2 B48394	major fat-globule

30	17	23.6	7	2 PD0029	pev-kinin 1 - pena
31	17	23.6	7	2 S57274	triacylglycerol li
32	17	23.6	7	2 S33244	neuromodulatory pe
33	17	23.6	7	2 S33245	neuromodulatory pe
34	17	23.6	7	2 S33246	neuromodulatory pe
35	17	23.6	8	2 PT0724	T-cell receptor be
36	17	23.6	8	2 JS0316	leucokinin VI - Ma
37	17	23.6	8	2 JS0317	leucokinin VII - M
38	17	23.6	8	2 JS0318	leucokinin VIII -
39	17	23.6	8	2 A31570	angiotensin-conver
40	17	23.6	9	2 A24244	adipokinetic hormo
41	17	23.6	9	2 PT0634	T-cell receptor be
42	17	23.6	9	2 PT0562	T-cell receptor be
43	17	23.6	9	2 A60522	sperm-activating p
44	17	23.6	10	2 B33995	hypotrehalosemic h
45	17	23.6	10	2 S08997	hypertrehalosemic

ALIGNMENTS

RESULT 1

S71868
glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)
N;Alternate names: Glutathione S-transferase class mu 4
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: S71868
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra
A;Reference number: S71864; MUID:96332484; PMID:8760377
A;Accession: S71868
A;Molecule type: protein
A;Residues: 1-10 <ROU>
A;Cross-references: UNIPROT:Q7M3E8
C;Comment: At least five species-independent classes of cytosolic glutathion transferase
s mitochondrial form are known.
C;Complex: dimer
C;Function:

A;Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
A;Pathway: detoxification; xenobiotics metabolism
A;Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
es of damage
C;Superfamily: glutathione transferase
C;Keywords: dimer; transferase

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4
|||
Db 4 GYW 6

RESULT 2

A35556
hypothetical protein (ODC region) - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C;Accession: A35556
R;Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosescu, J.; Almodovar, K.M.; Luk, G.D.
J. Biol. Chem. 265, 4884-4892, 1990
A;Title: Isolation and expression of a human ornithine decarboxylase gene.
A;Reference number: A35556; MUID:90202959; PMID:2318872
A;Accession: A35556
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <MOS>
A;Cross-references: GB:J05271

Query Match 33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYW 4
| | |
Db 5 CGAW 8

RESULT 3
PT0586
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0586
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
C;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
: | | |
Db 3 SIWG 6

RESULT 4
T17075
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)
C;Species: mitochondrion Chamaeleo fischeri
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17075
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene
A;Reference number: Z18674; MUID:97315309; PMID:9169559
A;Accession: T17075
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
C;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:g3603112; PID:g3603115; PIDN:AAC622
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 30.6%; Score 22; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 WLTIW 8
| | |
Db 2 WLLRW 6

RESULT 5
E41946
T-cell receptor gamma chain (1a.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: E41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: E41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <WHE>
C;Keywords: T-cell receptor

Query Match 29.2%; Score 21; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWL 5
| | |
Db 2 CAVWI 6

RESULT 6
JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric
, and of the circular muscle of the gastro-intestinal junction.

Query Match 27.8%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4
| : |
Db 1 GFW 3

RESULT 7
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: F41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-6 <WHE>
C;Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWL 5
| | |
Db 2 CAVWV 6

RESULT 8
S19288
acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase from K
A;Reference number: S19288; MUID:92109664; PMID:1764029
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>
A;Cross-references: UNIPROT:Q7M124

Query Match 27.8%; Score 20; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWL 5
| |:
Db 1 CNMNV 5

RESULT 9

PT0324
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0324
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0324
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
| |:
Db 3 GYGESYW 9

RESULT 10

PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0289
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 5.4e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WLTIWG 9
| |:
Db 4 WISMG 9

RESULT 11

E49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000

C;Accession: E49033; D49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
A;Accession: E49033
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <MOR>
A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A;Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)
A;Accession: D49033
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <MOR2>
A;Cross-references: GB:S72587; NID:g240696; PIDN:AAB20630.1; PID:g240697
A;Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)
C;Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYW 4
| |:
Db 1 CALW 4

RESULT 12

F49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C;Accession: F49033
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A;Title: Functionally distinct subsets of human gamma/delta T cells.
A;Reference number: A49033; MUID:92083926; PMID:1684157
A;Accession: F49033
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-10 <MOR>
A;Cross-references: GB:S72605; NID:g240700; PIDN:AAB20632.1; PID:g240701
A;Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIP:72606)
C;Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYW 4
| |:
Db 1 CALW 4

RESULT 13

C41946
T-cell receptor gamma chain (1t.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: C41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <WHE>
C;Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.4e+03;

Matches	2;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	CGYW	4						
Db	2	CAVW	5						
RESULT 14									
JS0315									
leucokinin V - Madeira cockroach									
C;Species: Leucophaea maderae (Madeira cockroach)									
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004									
C;Accession: JS0315									
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.									
Comp. Biochem. Physiol. C 88, 27-30, 1987									
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic									
A;Reference number: JS0315									
A;Accession: JS0315									
A;Molecule type: protein									
A;Residues: 1-8 <HOL>									
A;Cross-references: UNIPROT:P19987									
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act									
C;Keywords: amidated carboxyl end; cephalomyotropic peptide									
F;8/Modified site: amidated carboxyl end (Gly) #status experimental									
Query Match 25.0%; Score 18; DB 2; Length 8;									
Best Local Similarity 37.5%; Pred. No. 2.8e+05;									
Matches	3;	Conservative	1;	Mismatches	4;	Indels	0;	Gaps	0;
QY	2	GYWLTWIG	9						
			:						
Db	1	GSGFSSWG	8						
RESULT 15									
PT0230									
Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)									
C;Species: Homo sapiens (man)									
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996									
C;Accession: PT0230									
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.									
J. Exp. Med. 173, 395-407, 1991									
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j									
A;Reference number: PT0222; MUID:91108337; PMID:1899102									
A;Accession: PT0230									
A;Molecule type: DNA									
A;Residues: 1-10 <YAM>									
A;Experimental source: B lymphocyte									
C;Keywords: heterotetramer; immunoglobulin									
Query Match 25.0%; Score 18; DB 2; Length 10;									
Best Local Similarity 60.0%; Pred. No. 7.5e+03;									
Matches	3;	Conservative	2;	Mismatches	0;	Indels	0;	Gaps	0;
QY	5	LTWIG	9						
		: :							
Db	3	ITIFG	7						

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OM protein - protein search, using sw model

Run on: December 30, 2004, 14:22:33 ; Search time 100 seconds
(without alignments)
57.537 Million cell updates/sec

Title: US-10-046-922-35
Perfect score: 72
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	30.5	42.4	10	1	LABA_JATMU	P13270 jatropha mu
2	27	37.5	10	2	Q8SHF6	Q8shf6 chamaeleo m
3	26	36.1	8	2	Q70Y57	Q70y57 fuerstia af
4	26	36.1	8	2	CAD45547	Cad45547 fuerstia
5	24	33.3	10	2	Q7M3E8	Q7m3e8 sus scrofa
6	24	33.3	10	2	Q8SHN1	Q8shn1 bradypodion
7	24	33.3	10	2	Q6JL97	Q6jl97 neisseria g
8	24	33.3	10	2	AAS16521	Aas16521 neisseria
9	23.5	32.6	9	2	Q85DB0	Q85db0 lepilemur s
10	23.5	32.6	9	2	Q85DB8	Q85db8 lepilemur e
11	23.5	32.6	9	2	Q94NA9	Q94na9 daubentononia
12	23.5	32.6	9	2	Q94NB0	Q94nb0 microcebus
13	23.5	32.6	9	2	Q94NB1	Q94nb1 microcebus
14	23.5	32.6	9	2	Q94NB2	Q94nb2 microcebus
15	23.5	32.6	9	2	Q94XE6	Q94xe6 tectocoris
16	23	31.9	10	2	Q8SHC6	Q8shc6 furcifer be
17	22	30.6	10	2	O79912	O79912 chamaeleo f
18	22	30.6	10	2	Q9G697	Q9g697 chamaeleo d
19	22	30.6	10	2	Q8SH83	Q8sh83 brookesia t
20	22	30.6	10	2	Q8SH85	Q8sh85 brookesia t
21	22	30.6	10	2	Q8SH88	Q8sh88 brookesia t
22	22	30.6	10	2	Q8SH90	Q8sh90 brookesia s
23	22	30.6	10	2	Q8SH96	Q8sh96 brookesia p
24	22	30.6	10	2	Q8SHA2	Q8sha2 brookesia b
25	22	30.6	10	2	Q8SHA5	Q8sha5 brookesia a
26	22	30.6	10	2	Q8SHC9	Q8shc9 furcifer ba
27	22	30.6	10	2	Q8SHD2	Q8shd2 chamaeleo w
28	22	30.6	10	2	Q8SHD5	Q8shd5 chamaeleo s
29	22	30.6	10	2	Q8SHD8	Q8shd8 chamaeleo r
30	22	30.6	10	2	Q8SHE1	Q8she1 chamaeleo q
31	22	30.6	10	2	Q8SHE4	Q8she4 chamaeleo q

32	22	30.6	10	2	Q8SHE7	Q8she7 chamaeleo p
33	22	30.6	10	2	Q8SHF3	Q8shf3 chamaeleo m
34	22	30.6	10	2	Q8SHF9	Q8shf9 chamaeleo j
35	22	30.6	10	2	Q8SHG5	Q8shg5 chamaeleo h
36	22	30.6	10	2	Q8SHG8	Q8shg8 chamaeleo g
37	22	30.6	10	2	Q8SHH1	Q8shh1 chamaeleo f
38	22	30.6	10	2	Q8SHH4	Q8shh4 chamaeleo f
39	22	30.6	10	2	Q8SHH7	Q8shh7 chamaeleo e
40	22	30.6	10	2	Q8SHI0	Q8shi0 chamaeleo d
41	22	30.6	10	2	Q8SHI3	Q8shi3 chamaeleo c
42	22	30.6	10	2	Q8SHI6	Q8shi6 chamaeleo c
43	22	30.6	10	2	Q8SHI9	Q8shi9 chamaeleo c
44	22	30.6	10	2	Q8SHJ2	Q8shj2 chamaeleo a
45	22	30.6	10	2	Q8SHJ5	Q8shj5 calumma par

ALIGNMENTS

RESULT 1
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaeae;
OC Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
RT multifida L. (Euphorbiaceae). Isolation and sequence determination by
RT means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -|- FUNCTION: Labaditin is an active peptide which inhibits the
CC classical pathway of complement activation in vitro. Activity
CC seems to be based on an interaction with C1.
CC -|- PTM: This is a cyclic peptide.
CC -|- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
CC for treatment of infected wounds, skins infections and scabies.
KW Direct protein sequencing.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 42.4%; Score 30.5; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 GYWLTIWG 9
| | | | |
Db 2 GVM-TVWG 8

RESULT 2
Q8SHF6
ID Q8SHF6 PRELIMINARY; PRT; 10 AA.
AC Q8SHF6;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Chamaeleo melleri (Meller's chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OX NCBI_TaxID=179915;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169767; PubMed=12182400;
RA Townsend T., Larson A.;
RT "Molecular phylogenetics and mitochondrial genomic evolution in the
RT chamaeleonidae (Reptilia, Squamata).";
RL Mol. Phylogenet. Evol. 23:22-36(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448755; AAL90547.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1276 MW; 5E218E2733772727 CRC64;

Query Match 37.5%; Score 27; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 WLTIW 8
Db 2 WLLW 6

RESULT 3
Q70Y57
ID Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rp816;
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db 2 TIWG 5

RESULT 4
CAD45547
ID CAD45547 PRELIMINARY; PRT; 8 AA.
AC CAD45547;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db 2 TIWG 5

RESULT 5
Q7M3E8
ID Q7M3E8 PRELIMINARY; PRT; 10 AA.
AC Q7M3E8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE.
RA Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
RT "Characterization of pig liver glutathione S-transferases using HPLC-
RT electrospray-ionization mass spectrometry.";
RL Biochem. J. 317:879-884(1996).
DR PIR; S71868; S71868.
DR GO; GO:0004364; F:glutathione transferase activity; IEA.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1223 MW; 5E16395AB36B5877 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4
Db 4 GYW 6

RESULT 6
Q8SHN1
ID Q8SHN1 PRELIMINARY; PRT; 10 AA.
AC Q8SHN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bradypodion tavetanum (Dwarf Fischer's chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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GN RPS16.
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TIWG 9
Db 2 TIWG 5
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OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Brachyopodion.
OX NCBI_TaxID=179888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169767; PubMed=12182400;
RA Townsends T., Larson A.;
RT "Molecular phylogenetics and mitochondrial genomic evolution in the
RT chamaeleonidae (Reptilia, Squamata).";
RL Mol. Phylogenet. Evol. 23:22-36(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Townsends T.M., Larson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448730; AAL90472.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1327 MW; 5E2180C7336415B7 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTW 8
DB 2 WLSRW 6

RESULT 7
Q6JL97 PRELIMINARY; PRT; 10 AA.
AC Q6JL97;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NuOL (Fragment).
GN Name=nuOL;
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MS11;
RX PubMed=15084227;
RA Snyder L.A., Davies J.K., Saunders N.J.;
RT "Microarray genotyping of key experimental strains of Neisseria
RT gonorrhoeae reveals gene complement diversity and five new neisserial
RT genes associated with Minimal Mobile Elements.";
RL BMC Genomics 5:23-23(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MS11;
RX PubMed=15084227;
RA Snyder L.A., Davies J.K., Saunders N.J.;
RT "Microarray genotyping of key experimental strains of Neisseria
RT gonorrhoeae reveals gene complement diversity and five new neisserial
RT genes associated with Minimal Mobile Elements.";
RL BMC Genomics 5:23-23(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MS11;
RA Snyder L.A.S., Davies J.K., Saunders N.J.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY386266; AAS16521.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1227 MW; BACCB286379D1A6 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LTIWG 9
DB 3 MTFWG 7

RESULT 8
AAS16521 PRELIMINARY; PRT; 10 AA.
ID AAS16521
AC AAS16521;
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DT 20-MAY-2004 (TrEMBLrel. 27, Created)
DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE NuOL (Fragment).
GN NuOL.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MS11;
RX PubMed=15084227;
RA Snyder L.A., Davies J.K., Saunders N.J.;
RT "Microarray genotyping of key experimental strains of Neisseria
RT gonorrhoeae reveals gene complement diversity and five new neisserial
RT genes associated with Minimal Mobile Elements.";
RL BMC Genomics 5:23-23(2004).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MS11;
RA Snyder L.A.S., Davies J.K., Saunders N.J.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY386266; AAS16521.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1227 MW; BACCB286379D1A6 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 LTIWG 9
DB 3 MTFWG 7

RESULT 9
Q85DB0 PRELIMINARY; PRT; 9 AA.
ID Q85DB0
AC Q85DB0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Lepilemur septentrionalis (northern sportive lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
OX NCBI_TaxID=78584;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
RT lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224597; AAP33652.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1174 MW; 16C563636B5045B0 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTW 9
DB 5 YW---WG 8

RESULT 10
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Q85DB8
ID Q85DB8 PRELIMINARY; PRT; 9 AA.
AC Q85DB8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.
OX NCBI_TaxID=122230;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
DR EMBL; AF224595; AAP33644.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTIMG 9
Db || ||
5 YW---WG 8

RESULT 11
Q94NA9
ID Q94NA9 PRELIMINARY; PRT; 9 AA.
AC Q94NA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Daubentonia madagascariensis (Aye-aye).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;
OC Daubentonia.
OX NCBI_TaxID=31869;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22281620; PubMed=12393004;
RA Pastorini J., Forstner M.R., Martin R.D.;
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from mtDNA.";
RL J. Hum. Evol. 43:463-478 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
DR EMBL; AF224641; AAK70615.1; --
DR EMBL; AF224642; AAK70619.1; --

DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTIMG 9
Db || ||
5 YW---WG 8

RESULT 12
Q94NB0
ID Q94NB0 PRELIMINARY; PRT; 9 AA.
AC Q94NB0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Microcebus rufus (Brown mouse lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=122232;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates) based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884 (2003).
DR EMBL; AF224636; AAK70595.1; --
DR EMBL; AF224637; AAK70599.1; --
DR EMBL; AF224638; AAK70603.1; --
DR EMBL; AF224639; AAK70607.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTIMG 9
Db || ||
5 YW---WG 8

RESULT 13
Q94NB1
ID Q94NB1 PRELIMINARY; PRT; 9 AA.
AC Q94NB1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Microcebus ravelobensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirrhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=122231;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224630; AAK70571.1; -.
DR EMBL; AF224631; AAK70575.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 3 YWLTWIG 9
Db 5 YW---WG 8

RESULT 14
Q94NB2 ID Q94NB2 PRELIMINARY; PRT; 9 AA.
AC Q94NB2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COIII;
OS Microcebus murinus (Lesser mouse lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)
based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224624; AAK70547.1; -.
DR EMBL; AF224625; AAK70551.1; -.
DR EMBL; AF224626; AAK70555.1; -.
DR EMBL; AF224627; AAK70559.1; -.
DR EMBL; AF224628; AAK70563.1; -.
DR EMBL; AF224629; AAK70567.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 3 YWLTWIG 9
Db 5 YW---WG 8

RESULT 15
Q94XE6 ID Q94XE6 PRELIMINARY; PRT; 9 AA.
AC Q94XE6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit III (Fragment).
GN Name=cox3;
OS Tectocoris diophthalmus (cotton harlequin bug).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Tectocoris.
OX NCBI_TaxID=159956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396409; PubMed=11504862;
RA Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
RT "Increased rate of gene rearrangement in the mitochondrial genomes of
three orders of hemipteroid insects.";
RL Mol. Biol. Evol. 18:1828-1832(2001).
DR EMBL; AF335990; AAK55283.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 3 YWLTWIG 9
Db 5 YW---WG 8

Search completed: December 30, 2004, 14:43:05
Job time : 100 secs

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OM protein - protein search, using sw model

Run on: January 3, 2005, 11:51:33 ; Search time 150 Seconds
(without alignments)
19.132 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywlting 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	5	ABP53931 VEGFR-3 b
2	54	100.0	10	5	ABP53932 VEGFR-3 b
3	43	79.6	13	6	AAO26093 Fc region
4	43	79.6	13	8	ADJ50760 Human ser
5	43	79.6	474	6	ABU30004 Protein e
6	43	79.6	492	7	ADC97318 E. faeciu
7	42	77.8	120	4	AAB62747 Human HIV
8	42	77.8	1140	4	AAE09365 Human ATP
9	42	77.8	1498	4	AAE09362 Mouse ATP
10	42	77.8	1503	2	AAY43544 A human M
11	42	77.8	1503	4	AAE09361 Human ATP
12	42	77.8	1503	4	AAE09370 Human ATP
13	42	77.8	1503	4	AAE09367 Human ATP
14	42	77.8	1503	4	AAE09368 Human ATP
15	42	77.8	1503	4	AAE09369 Human ATP
16	42	77.8	1503	4	AAE09364 Human ATP
17	42	77.8	1503	4	AAE09371 Human ATP
18	42	77.8	1503	4	AAE09363 Human ATP
19	42	77.8	1503	5	ABP52113 Homo sapi
20	41	75.9	14	6	AAO26134 Fc region
21	41	75.9	14	8	ADJ50801 Human ser
22	41	75.9	34	4	ABB38460 Peptide #
23	41	75.9	34	4	AAM31901 Peptide #
24	41	75.9	34	4	AAM71604 Human bon
25	41	75.9	34	4	AAM59071 Human bra

26	41	75.9	34	4	ABG53286	Abg53286 Human liv
27	41	75.9	34	5	ABG41416	Abg41416 Human pep
28	41	75.9	222	2	AAY00213	Aay00213 Enterococ
29	41	75.9	222	5	ABP43432	Abp43432 E faecali
30	41	75.9	222	6	ABU88460	Abu88460 E. faecal
31	41	75.9	222	6	ABU13711	Abu13711 Enterococ
32	41	75.9	229	7	ADH85745	Adh85745 Enterococ
33	41	75.9	266	2	AAY00212	Aay00212 Enterococ
34	41	75.9	266	5	ABP43431	Abp43431 E faecali
35	41	75.9	266	6	ABU88459	Abu88459 E. faecal
36	41	75.9	266	6	ABU13710	Abu13710 Enterococ
37	41	75.9	567	8	ADN46152	Adn46152 Thermococ
38	40	74.1	116	2	AAR15437	Aar15437 Heavy cha
39	40	74.1	116	6	ABO27261	ABO27261 ICAM-1 bi
40	40	74.1	116	6	ABO27269	ABO27269 ICAM-1 bi
41	40	74.1	116	6	ABO27263	ABO27263 ICAM-1 bi
42	40	74.1	116	6	ABO27259	ABO27259 ICAM-1 bi
43	40	74.1	116	6	ABO27255	ABO27255 ICAM-1 bi
44	40	74.1	116	6	ABO27277	ABO27277 Humanised
45	40	74.1	116	6	ABO27273	ABO27273 Murine 1A

ALIGNMENTS

RESULT 1
ABP53931
ID ABP53931 standard; peptide; 10 AA.
XX
AC ABP53931;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:34.
XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnery; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Misc-difference 1 /note= "any amino acid"
FT Misc-difference 10 /note= "any amino acid"
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB0000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX

PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX

PS Claim 12; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and
CC

CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
Db 2 GYWLTIWG 9

RESULT 2
ABP53932
ID ABP53932 standard; peptide; 10 AA.
XX
AC ABP53932;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:35.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnerary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
XX WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 13; Page 80; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
Db 2 GYWLTIWG 9

RESULT 3
AAO26093
ID AAO26093 standard; peptide; 13 AA.
XX
AC AAO26093;
XX
DT 03-APR-2003 (first entry)
XX
DE Fc region binding peptide SEQ ID No 73.
XX
KW Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;
KW antibody response; half-life; stability; circulatory system.
XX
OS Unidentified.
XX
PN WO200286070-A2.
XX
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US012492.
XX
PR 18-APR-2001; 2001US-0284534P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Wu Q, Ley AC, Stochl M, Ransohoff TC, Potter MD;
XX
XX WPI; 2003-201220/19.
XX
PT New polypeptides, useful as binding molecules for detecting, isolating or
PT purifying immunoglobulin Fc-region polypeptides present in a solution, or
PT for regulating or preventing an antibody response.
XX
PS Claim 3; Page 76; 152pp; English.
XX
CC The invention relates to novel isolated polypeptides comprising a
CC sequence that binds an immunoglobulin Fc region. The polypeptides are
CC useful as binding molecules for detecting, isolating or purifying
CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole
CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are
CC also useful for regulating or preventing an antibody response, or for
CC increasing the half-life and over all stability of a therapeutic or
CC diagnostic compound that is administered to or enters the circulatory
CC system of an individual. This sequence represents an Fc region binding
CC peptide of the invention
XX
SQ Sequence 13 AA;

Query Match 79.6%; Score 43; DB 6; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
 :||| :||

. Db 1 GYWCNVWG 8

RESULT 4
ADJ50760
ID ADJ50760 standard; peptide; 13 AA.
XX
AC ADJ50760;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human serum albumin binding peptide, Seq ID No 297.
XX
KW human serum albumin; HSA; serum; blood; tumour; human.
XX
OS Homo sapiens.
XX
PN WO2003106493-A1.
XX
PD 24-DEC-2003.
XX
PF 16-JUN-2003; 2003WO-US018896.
XX
PR 14-JUN-2002; 2002US-0388642P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Sato AK, Dawson BM;
XX
DR WPI; 2004-082161/08.
XX
PT Evaluating sample comprising soluble serum protein by forming complex
PT comprising serum protein and physically associated compounds using
PT peptide ligand that specifically binds with proteins, which is separated
PT and evaluated.
XX
PS Disclosure; SEQ ID NO 297; 191pp; English.
XX
CC The invention relates to a method of evaluating sample by providing a
CC soluble serum protein (I), one or more compounds physically associated
CC with (I), and a (I)-binding agent that comprises a peptide that
CC specifically binds to (I), allowing the (I)-binding agent to bind to (I)
CC to form a complex including one or more compounds physically associated
CC with (I), separating the complex from one or more components of the
CC sample, and evaluating one or more of the physically associated
CC compounds. The sample comprises blood or serum, or is obtained from a
CC biopsy. The sample may also be obtained from a tumour or a region within
CC 5 mm of a tumour. The method is useful for detecting modulators that
CC modulate interaction of serum protein-binding compound and serum protein
CC and for identifying binding ligands for serum protein. The present
CC sequence represents a serum albumin-binding peptide identified using the
CC method of the invention.
XX
SQ Sequence 13 AA;
Query Match 79.6%; Score 43; DB 8; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYWLTIWG 8
|||:|
Db 1 GYWCNVWG 8

RESULT 5
ABU30004
ID ABU30004 standard; protein; 474 AA.
XX
AC ABU30004;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #15531.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Enterococcus faecium.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA33874.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 57928; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 474 AA;

Query Match 79.6%; Score 43; DB 6; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYWLTIW 7
|||
Db 94 GYWLTCW 100

RESULT 6
ADC97318
ID ADC97318 standard; protein; 492 AA.
XX
AC ADC97318;
XX
DT 01-JAN-2004 (first entry)
XX
DE E. faecium protein sequence SEQ ID 6945.
XX
KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
XX abdominal-pelvic infection.
OS Enterococcus faecium.
XX
PN US6583275-B1.
XX
PD 24-JUN-2003.
XX
PF 30-JUN-1998; 98US-00107532.
XX
PR 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2003-799836/75.
DR N-PSDB; ADC93664.
XX
PS New isolated nucleic acid derived from Enterococcus faecium encoding an
XX Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
PS Example 1; SEQ ID NO 6945; 243pp; English.
XX
CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX
SQ Sequence 492 AA;
Query Match 79.6%; Score 43; DB 7; Length 492;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GYWLTIW 7
Db 112 GYWLTCW 118
RESULT 7
AAB62747
ID AAB62747 standard; protein; 120 AA.
XX

AAB62747;
AC
XX
DT 03-APR-2001 (first entry)
XX
DE Human HIV-1 monoclonal antibody SEQ ID NO: 46.
XX
KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
KW envelope glycoprotein; gpl20; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200100678-A1.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-US017327.
XX
PR 30-JUN-1999; 99US-0141701P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Watkins BA, Reitz MS;
XX
DR WPI; 2001-112438/12.
DR N-PSDB; AAF29048.
XX
PT Novel human monoclonal antibody immunoreactive with human
PT immunodeficiency virus-1 glycoprotein gpl20, useful for detecting HIV-1
PT in biological sample and providing passive immunotherapy to HIV-1
PT infected mammal.
XX
PS Claim 1; Page 51-52; 81pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC variable regions of human monoclonal antibodies which are immunoreactive
CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
CC These can be used in diagnosis and therapy of HIV-1 infection
XX
SQ Sequence 120 AA;
Query Match 77.8%; Score 42; DB 4; Length 120;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GYWLTIWG 8
Db 104 GYWVSYWG 111
RESULT 8
AAE09365
ID AAE09365 standard; protein; 1140 AA.
XX
AC AAE09365;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6, MRP6 truncated mutant.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200162977-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.

XX 23-FEB-2000; 2000US-0184269P.
PR (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
XX
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX
XX WPI; 2001-536645/59.
DR N-PSDB; AAD16258.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
XX Claim 10; Page; 163pp; English.
XX
XX The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane- spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in
CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) truncated mutant which is obtained as the
CC result of a stop codon at position 1141 of MRP6 protein. Note: The
CC present sequence is not shown in the specification but is derived from
CC human ATP-binding cassette transporter ABCC6 (MRP6) protein [SED ID NO:
CC 3] shown in figure 3 of the specification (AAE09361)
XX
SQ Sequence 1140 AA;

Query Match 77.8%; Score 42; DB 4; Length 1140;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
|||:|
DB 965 GYWLTLW 971

RESULT 9
AAE09362
ID AAE09362 standard; protein; 1498 AA.
XX
AC AAE09362;
XX
DT 19-NOV-2001 (first entry)
XX
DE Mouse ATP-binding cassette transporter ABCC6 (MRP6) protein.
XX
KW Mouse; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
XX
OS Mus musculus.
XX
PN WO200162977-A2.
XX

PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.
XX
PR 23-FEB-2000; 2000US-0184269P.
XX
XX (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX
XX WPI; 2001-536645/59.
DR N-PSDB; AAD16236.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
XX Example 5; Page 152-159; 163pp; English.
PS
XX
XX The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane- spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in
CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is mouse ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since
CC ABCC6 protein is involved in drug-resistance it is also called Multidrug
CC Resistance associated protein 6 (MRP6)
XX
SQ Sequence 1498 AA;

Query Match 77.8%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
|||:|
DB 960 GYWLTLW 966

RESULT 10
AA43544
ID AA43544 standard; protein; 1503 AA.
XX
AC AA43544;
XX
DT 26-JAN-2000 (first entry)
XX
DE A human MPR-related ABC transporter designated MOAT-E.
XX
KW Human; MPR-related ABC transporter; MOAT protein; MOAT-E;
KW MOAT mediated transport; anticancer drug sensitivity;
KW transporter mediated cellular efflux; anticancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1215

FT /note= "encoded by ACT"
FT Misc-difference 1274
FT /note= "encoded by TGC"
FT Misc-difference 1287
FT /note= "encoded by TTC"
FT Misc-difference 1455
FT /note= "encoded by CCC"
XX
PN WO9949735-A1.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006644.
XX
PR 27-MAR-1998; 98US-0079759P.
PR 03-AUG-1998; 98US-0095153P.
XX
PA (FOXC-) FOX CHASE CANCER CENT.
XX
PI Kruh G, Lee K, Belinsky M, Bain L;
XX
DR WPI; 1999-610812/52.
DR N-PSDB; AAZ30081.
XX
PT New transporter gene useful for screening for anti-cancer drugs.
XX
PS Claim 39; Page 144-147; 153pp; English.
XX
CC The present sequence represents a human MPR-related ABC transporter
CC (MOAT) protein, designated MOAT-E. The protein comprises a multi-domain
CC structure including a tandem repeat of nucleotide binding folds appended
CC C-terminal to a hydrophobic domain, having Walker A and B ATP binding
CC sites and several potential membrane spanning domains. The MOAT nucleic
CC acids are useful for screening a test compound for inhibition of MOAT
CC mediated transport, indicated by restoration of anticancer drug
CC sensitivity, which in turn causes a reduction of transporter mediated
CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
CC probes to detect the presence or expression of genes encoding MOAT
CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
CC MOAT proteins
XX
SQ Sequence 1503 AA;

Query Match 77.8%; Score 42; DB 2; Length 1503;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
Db 965 GYWLSLW 971

RESULT 11
AAE09361
ID AAE09361 standard; protein; 1503 AA.
XX
AC AAE09361;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6 (MRP6) protein.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 656. .679
FT /note= "Nucleotide binding fold-1 (NFB-1) region"
FT 747. .768

FT /note= "Nucleotide binding fold-1 (NFB-1) region"
FT 775. .784
FT /note= "Nucleotide binding fold-1 (NFB-1) region"
FT 1292. .1307
FT /note= "Nucleotide binding fold-2 (NFB-2) region"
FT 1321. .1327
FT /note= "Nucleotide binding fold-2 (NFB-2) region"
FT 1403. .1433
FT /note= "Nucleotide binding fold-2 (NFB-2) region"
XX
PN WO200162977-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.
XX
PR 23-FEB-2000; 2000US-0184269P.
XX
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
PI Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;
XX
DR WPI; 2001-536645/59.
DR N-PSDB; AAD16230, AAD16231.
XX
PT Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
PS Example 2; Fig 3; 163pp; English.
XX
CC The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane- spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in
CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since
CC ABCC6 protein is involved in drug-resistance it is also called Multidrug
CC Resistance associated protein 6 (MRP6)
XX
SQ Sequence 1503 AA;

Query Match 77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
Db 965 GYWLSLW 971

RESULT 12
AAE09370
ID AAE09370 standard; protein; 1503 AA.
XX
AC AAE09370;
XX

DT 19-NOV-2001 (first entry)
DE Human ATP-binding cassette transporter ABCC6 (MRP6) R1314W mutant.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; munein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1314
FT /note= "Wild type Arg substituted with Trp"
XX
PN WO200162977-A2.
XX
XX 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.
XX
PR 23-FEB-2000; 2000US-0184269P.
XX
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
XX Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX
DR WPI; 2001-536645/59.
DR N-PSDB; AAD16263.
XX
PT Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
PS Claim 13; Page; 163pp; English.
XX
CC The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane- spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in
CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) R1314W mutant protein. Note: The present
CC sequence is not shown in the specification but is derived from human ATP-
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in
CC figure 3 of the specification (AAE09361)
XX
SQ Sequence 1503 AA;
Query Match 77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWLTIW 7
Db 965 GYWLTLW 971

RESULT 13
AAE09367
ID AAE09367 standard; protein; 1503 AA.
XX
XX AAE09367;
AC
XX 19-NOV-2001 (first entry)
XX
DE Human ATP-binding cassette transporter ABCC6 (MRP6) V1298F mutant.
XX
KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
KW Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
KW mutant; munein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1298
FT /note= "Wild type Val substituted with Phe"
XX
PN WO200162977-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005741.
XX
PR 23-FEB-2000; 2000US-0184269P.
XX
PA (PXEI-) PXE INT INC.
PA (UYHA-) UNIV HAWAII.
XX
PI Boyd CD, Csiszar K, Lesaux O, Urban Z, Terry S;
XX
DR WPI; 2001-536645/59.
DR N-PSDB; AAD16260.
XX
PT Screening presence of Pseudoxanthoma elasticum mutation useful for
PT identifying homozygotes, compound heterozygotes or carriers involves
PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
PS Claim 13; Page; 163pp; English.
XX
CC The invention relates to methods and compositions for diagnosing and
CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
CC dysfunctions. The invention is useful for screening for the presence of a
CC PXE mutation. Mutations associated with PXE maps to the ATP-binding
CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
CC protein located in the plasma membrane containing 17 membrane- spanning
CC helices grouped into three transmembrane domains. PXE is inherited as an
CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
CC a heritable disorder characterised by mineralisation of elastic fibers in
CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) V1298F mutant protein. Note: The present
CC sequence is not shown in the specification but is derived from human ATP-
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in
CC figure 3 of the specification (AAE09361)
XX
SQ Sequence 1503 AA;

CC skin, arteries and the retina, that result in dermal lesions with
CC associated laxity and loss of elasticity, arterial insufficiency,
CC cardiovascular disease and retinal haemorrhages leading to macular
CC degeneration. The method is useful for screening a population of
CC individuals in order to identify individuals with one or more PXE
CC associated MRP6 alleles who are then provided with appropriate genetic
CC counselling in view of the PXE status. The methods are useful for
CC identifying homozygotes, compound heterozygotes or carriers and thus are
CC useful in the area of genetic testing, carrier detection and prenatal
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)
CC transporter, ABCC6 (MRP6) A1303P mutant protein. Note: The present
CC sequence is not shown in the specification but is derived from human ATP-
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in
CC figure 3 of the specification (AAE09361)
XX
SQ Sequence 1503 AA;

Query Match 77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
| | | | : |
Db 965 GYWLTLW 971

Search completed: January 3, 2005, 12:09:53
Job time : 153 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:06:49 ; Search time 38 Seconds
(without alignments)
13.962 Million cell updates/sec

Title: SEQ32

Perfect score: 54

Sequence: 1 gywltiwg'8

Scoring table: BLOSUM62

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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	492	4	US-09-107-532A-6945
2	42	77.8	1498	4	US-09-792-616-9
3	42	77.8	1503	4	US-09-792-616-3
4	41	75.9	222	4	US-09-071-035-408
5	41	75.9	229	4	US-09-134-000C-3630
6	41	75.9	266	4	US-09-071-035-406
7	40	74.1	668	4	US-09-248-796A-19350
8	39	72.2	478	4	US-09-107-532A-6868
9	38	70.4	328	4	US-09-540-236-2629
10	37	68.5	24	4	US-09-270-767-41173
11	37	68.5	24	4	US-09-270-767-56389
12	37	68.5	132	4	US-09-248-796A-22785
13	37	68.5	278	4	US-09-145-828A-11
14	37	68.5	278	4	US-09-903-456-18
15	37	68.5	499	4	US-09-252-991A-23328
16	37	68.5	591	4	US-09-561-077C-18
17	37	68.5	591	4	US-09-221-014-18
18	37	68.5	865	4	US-09-252-991A-19339
19	36.5	67.6	612	4	US-09-252-991A-19134
20	36	66.7	119	2	US-08-318-157B-5
21	36	66.7	119	4	US-09-253-794-5
22	36	66.7	172	4	US-09-107-532A-6560
23	36	66.7	219	3	US-09-247-373B-52
24	36	66.7	242	2	US-08-512-955-4
25	36	66.7	247	4	US-09-252-991A-26736
26	36	66.7	268	2	US-08-861-512-3
27	36	66.7	280	1	US-08-414-685-2

28	36	66.7	367	4	US-09-248-796A-15188	Sequence 15188, A
29	36	66.7	1528	1	US-08-463-092B-6	Sequence 6, Appli
30	36	66.7	1528	2	US-08-462-109A-6	Sequence 6, Appli
31	36	66.7	1528	2	US-08-460-907B-6	Sequence 6, Appli
32	36	66.7	1528	3	US-08-463-179A-6	Sequence 6, Appli
33	36	66.7	1528	3	US-08-461-384B-6	Sequence 6, Appli
34	36	66.7	1531	1	US-08-141-893-2	Sequence 2, Appli
35	36	66.7	1531	1	US-08-463-092B-2	Sequence 2, Appli
36	36	66.7	1531	1	US-08-463-092B-4	Sequence 4, Appli
37	36	66.7	1531	2	US-08-462-109A-2	Sequence 2, Appli
38	36	66.7	1531	2	US-08-462-109A-4	Sequence 2, Appli
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40	36	66.7	1531	2	US-08-460-907B-4	Sequence 2, Appli
41	36	66.7	1531	3	US-08-463-179A-2	Sequence 2, Appli
42	36	66.7	1531	3	US-08-463-179A-4	Sequence 4, Appli
43	36	66.7	1531	3	US-08-461-384B-2	Sequence 2, Appli
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45	36	66.7	1531	3	US-08-407-207A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-107-532A-6945
; Sequence 6945, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6945:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...492
SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945


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Query Match      79.6%; Score 43; DB 4; Length 492;
Best Local Similarity 85.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYWLTIW 7
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Db      112 GYWLTCW 118

RESULT 2
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: Pseudoxanthoma Elasticum
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match      77.8%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYWLTIW 7
      |||||
Db      960 GYWLSLW 966

RESULT 3
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: Pseudoxanthoma Elasticum
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      77.8%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYWLTIW 7
      |||||
Db      965 GYWLSLW 971

RESULT 4
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
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; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-035-408
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Query Match      75.9%; Score 41; DB 4; Length 222;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYWLTIW 8
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Db      179 GTWITLW 186
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RESULT 5
US-09-134-000C-3630
; Sequence 3630, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3630
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630
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Query Match      75.9%; Score 41; DB 4; Length 229;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYWLTIW 8
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RESULT 9
US-09-540-236-2629
; Sequence 2629, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2629
; LENGTH: 328
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2629

Query Match 70.4%; Score 38; DB 4; Length 328;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
| |||||
Db 116 GQWLTW 122

RESULT 10
US-09-270-767-41173
; Sequence 41173, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41173
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41173

Query Match 68.5%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWLTIWG 8
: ||::||
Db 16 HWLSLWG 22

RESULT 11
US-09-270-767-56389
; Sequence 56389, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56389
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56389

Query Match 68.5%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWLTIWG 8
: ||::||
Db 16 HWLSLWG 22

RESULT 12
US-09-248-796A-22785
; Sequence 22785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22785
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (6), (77), (85)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-22785

Query Match 68.5%; Score 37; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTI 6
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Db 123 GYWLTI 128

RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.O1
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match 68.5%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7

Job time : 39 secs

Db 108 GYWIFLW 114

RESULT 14
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match 68.5%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 108 GYWIFLW 114

RESULT 15
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match 68.5%; Score 37; DB 4; Length 499;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 111 GYWISAW 117

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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:13:15 ; Search time 142 Seconds
(without alignments)
20.266 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywltiWG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	13	US-10-046-922-34
2	54	100.0	10	13	US-10-046-922-35
3	43	79.6	13	14	US-10-125-869A-73
4	43	79.6	13	15	US-10-462-262-297
5	43	79.6	474	15	US-10-282-122A-57928
6	43	79.6	671	16	US-10-437-963-190740
7	42	77.8	1498	10	US-09-792-616-9
8	42	77.8	1498	16	US-10-764-328-9
9	42	77.8	1503	10	US-09-792-616-3
10	42	77.8	1503	16	US-10-764-328-3
11	41	75.9	14	14	US-10-125-869A-114
12	41	75.9	14	15	US-10-462-262-338
13	41	75.9	34	9	US-09-864-761-43458
					Sequence 34, Appl
					Sequence 35, Appl
					Sequence 73, Appl
					Sequence 297, App
					Sequence 57928, A
					Sequence 190740,
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 3, Appli
					Sequence 3, Appli
					Sequence 114, App
					Sequence 338, App
					Sequence 43458, A

14	41	75.9	82	15	US-10-424-599-240891	Sequence 240891,
15	41	75.9	222	9	US-09-071-035-408	Sequence 408, App
16	41	75.9	222	14	US-10-206-576-408	Sequence 408, App
17	41	75.9	266	9	US-09-071-035-406	Sequence 406, App
18	41	75.9	266	14	US-10-206-576-406	Sequence 406, App
19	40	74.1	101	15	US-10-424-599-194869	Sequence 194869,
20	40	74.1	116	10	US-09-910-483-1	Sequence 1, Appli
21	40	74.1	116	10	US-09-910-483-5	Sequence 5, Appli
22	40	74.1	116	10	US-09-910-483-9	Sequence 9, Appli
23	40	74.1	116	10	US-09-910-483-13	Sequence 13, Appl
24	40	74.1	116	10	US-09-910-483-17	Sequence 17, Appl
25	40	74.1	116	10	US-09-910-483-21	Sequence 21, Appl
26	40	74.1	116	10	US-09-910-483-25	Sequence 25, Appl
27	40	74.1	116	10	US-09-910-483-29	Sequence 29, Appl
28	40	74.1	116	10	US-09-910-483-33	Sequence 33, Appl
29	40	74.1	116	10	US-09-910-483-37	Sequence 37, Appl
30	40	74.1	116	10	US-09-910-483-41	Sequence 41, Appl
31	40	74.1	116	10	US-09-910-483-43	Sequence 43, Appl
32	40	74.1	138	14	US-10-160-232-86	Sequence 86, Appl
33	40	74.1	138	14	US-10-160-232-90	Sequence 90, Appl
34	40	74.1	373	14	US-10-369-493-8834	Sequence 8834, Ap
35	39	72.2	13	14	US-10-125-869A-75	Sequence 75, Appl
36	39	72.2	13	15	US-10-462-262-299	Sequence 299, App
37	39	72.2	57	15	US-10-424-599-226815	Sequence 226815,
38	39	72.2	86	17	US-10-425-115-188067	Sequence 188067,
39	39	72.2	91	14	US-10-156-761-13764	Sequence 13764, A
40	39	72.2	162	9	US-09-738-626-5178	Sequence 5178, Ap
41	39	72.2	452	14	US-10-091-007-88	Sequence 88, Appl
42	39	72.2	474	15	US-10-282-122A-52805	Sequence 52805, A
43	39	72.2	475	15	US-10-282-122A-57680	Sequence 57680, A
44	39	72.2	794	9	US-09-738-626-4579	Sequence 4579, Ap
45	38.5	71.3	101	17	US-10-425-115-260407	Sequence 260407,

ALIGNMENTS

RESULT 1
US-10-046-922-34
; Sequence 34, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)..(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match 100.0%; Score 54; DB 13; Length 10;
Best local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
Db 2 GYWLTIWG 9

RESULT 2
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide

US-10-046-922-35
Query Match 100.0%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWLTIWG 8
Db 2 GYWLTIWG 9

US-10-125-869A-73
; Sequence 73, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ranschoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide

US-10-125-869A-73
Query Match 79.6%; Score 43; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYWLTIWG 8
Db 1 GYWCNVWG 8

US-10-462-262-297
; Sequence 297, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.

US-10-462-262-297
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide

US-10-462-262-297
Query Match 79.6%; Score 43; DB 15; Length 13;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYWLTIWG 8
Db 1 GYWCNVWG 8

US-10-282-122A-57928
; Sequence 57928, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

US-10-282-122A-57928
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57928
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Enterococcus faecium

US-10-125-869A-73
Query Match 79.6%; Score 43; DB 14; Length 13;
Best Local Similarity 62.5%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 GYWLTIWG 8
Db 1 GYWCNVWG 8

US-10-462-262-297
; Sequence 297, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.

US-10-282-122A-57928

Query Match 79.6%; Score 43; DB 15; Length 474;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
|||||
Db 94 GYWLTCW 100

RESULT 6

US-10-437-963-190740
; Sequence 190740, Application US/10437963
; Publication No. US20040123343A1

GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 190740

; LENGTH: 671

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_87125C.1.1.pep

US-10-437-963-190740

Query Match 79.6%; Score 43; DB 16; Length 671;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWLTIWG 8
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Db 329 YWTTIWG 335

RESULT 7

US-09-792-616-9
; Sequence 9, Application US/09792616
; Publication No. US20030165828A1

GENERAL INFORMATION:

; APPLICANT: PXE International, Inc.

; APPLICANT: University of Hawaii

; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing

; TITLE OF INVENTION: Pseudoxanthoma Elasticum

; FILE REFERENCE: PXE-001

; CURRENT APPLICATION NUMBER: US/09/792,616

; CURRENT FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 1498

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-792-616-9

Query Match 77.8%; Score 42; DB 10; Length 1498;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
|||||

Db 960 GYWLSLW 966

RESULT 8

US-10-764-328-9
; Sequence 9, Application US/10764328
; Publication No. US20040166521A1

GENERAL INFORMATION:

; APPLICANT: PXE International, Inc.

; APPLICANT: University of Hawaii

; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing

; FILE REFERENCE: PXE-001PC

; CURRENT APPLICATION NUMBER: US/10/764,328

; CURRENT FILING DATE: 2004-01-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 9

; LENGTH: 1498

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-764-328-9

Query Match 77.8%; Score 42; DB 16; Length 1498;

Best Local Similarity 71.4%; Pred. No. 9.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7

|||||

Db 960 GYWLSLW 966

RESULT 9

US-09-792-616-3

; Sequence 3, Application US/09792616

; Publication No. US20030165828A1

GENERAL INFORMATION:

; APPLICANT: PXE International, Inc.

; APPLICANT: University of Hawaii

; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing

; TITLE OF INVENTION: Pseudoxanthoma Elasticum

; FILE REFERENCE: PXE-001

; CURRENT APPLICATION NUMBER: US/09/792,616

; CURRENT FILING DATE: 2001-02-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 1503

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-792-616-3

Query Match 77.8%; Score 42; DB 10; Length 1503;

Best Local Similarity 71.4%; Pred. No. 9.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7

|||||

Db 965 GYWLSLW 971

RESULT 10

US-10-764-328-3

; Sequence 3, Application US/10764328

; Publication No. US20040166521A1

GENERAL INFORMATION:

; APPLICANT: PXE International, Inc.

; APPLICANT: University of Hawaii

; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing

; TITLE OF INVENTION: Pseudoxanthoma Elasticum

; FILE REFERENCE: PXE-001PC

; CURRENT APPLICATION NUMBER: US/10/764,328

; CURRENT FILING DATE: 2004-01-23

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3

Query Match      77.8%; Score 42; DB 16; Length 1503;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
      |||||::|
Db      965 GYWLSLW 971

RESULT 11
US-10-125-869A-114
; Sequence 114, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-114

Query Match      75.9%; Score 41; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWLTIW 8
      |||||
Db      1 GFWCTFWG 8

RESULT 12
US-10-462-262-338
; Sequence 338, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-338

Query Match      75.9%; Score 41; DB 15; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GYWLTIW 8
      |||||
Db      1 GFWCTFWG 8

RESULT 13
US-09-864-761-43458
; Sequence 43458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43458
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
```



```
;
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
US-09-864-761-43458

Query Match      75.9%; Score 41; DB 9; Length 34;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
      |||:|:|
Db      25 GYWITVFG 32

RESULT 14
US-10-424-599-240891
; Sequence 240891, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240891
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(82)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59551C.1.pep
US-10-424-599-240891

Query Match      75.9%; Score 41; DB 15; Length 82;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYWLTIW 7
      ||||:|
Db      76 GYWLNLW 82

RESULT 15
US-09-071-035-408
; Sequence 408, Application US/09071035
; Publication No. US20020045737A1
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Hp Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
```

```
;
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-408

Query Match      75.9%; Score 41; DB 9; Length 222;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 GYWLTIWG 8
      |||:|:|
Db      179 GTWITLWG 186

Search completed: January 3, 2005, 12:25:21
Job time : 143 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:03:34 ; Search time 38 Seconds
(without alignments)
20.256 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywlting 8
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	77.8	441	2 C95307	probable transport
2	42	77.8	1502	2 T42216	multidrug resistan
3	41	75.9	391	2 PC4117	replication protei
4	41	75.9	419	2 E90446	permease [imported
5	40	74.1	142	2 C34903	Ig heavy chain pre
6	40	74.1	425	2 B71038	probable Na+/H+-ex
7	40	74.1	508	2 C95282	probable ABC trans
8	39	72.2	376	2 AF1978	hypothetical prote
9	39	72.2	475	2 T46745	arginine/ornithine
10	39	72.2	490	2 C86879	arginine/ornithine
11	38	70.4	118	2 T35739	probable integral
12	38	70.4	426	2 C75176	na+/h+ antiporter
13	38	70.4	477	2 G90251	ABCtransporter [im
14	38	70.4	583	2 T50103	probable oxidoredu
15	38	70.4	829	2 S58888	ins p4-binding pro
16	38	70.4	829	2 S71847	ins p4-binding pro
17	37.5	69.4	1063	2 A33830	cation efflux syst
18	37.5	69.4	1063	2 JC4700	cadmium, zinc, cob
19	37	68.5	123	1 AVMS14	Ig heavy chain v r
20	37	68.5	167	2 AF0881	probable exported
21	37	68.5	172	2 AI2232	hypothetical prote
22	37	68.5	187	1 S13868	ubiquinol-cytochro
23	37	68.5	197	2 AF2356	hypothetical prote
24	37	68.5	218	2 S76385	hypothetical prote
25	37	68.5	286	2 E88690	protein F41H10.7 [
26	37	68.5	292	2 S49164	LysR-type protein
27	37	68.5	360	2 S74751	CDP-glucose 4,6-de
28	37	68.5	380	2 S12839	Ig heavy chain pre
29	37	68.5	416	2 AF1127	rod shape-determin

30	37	68.5	472	2 E83497	probable amino aci
31	37	68.5	482	2 JH0110	arginine/ornithine
32	37	68.5	497	2 G86878	arginine/ornithine
33	36.5	67.6	607	2 F82966	probable transcarb
34	36	66.7	164	2 F69990	hypothetical prote
35	36	66.7	171	2 E83140	phosphatidylglycer
36	36	66.7	239	2 H85756	partial probable m
37	36	66.7	241	2 G82391	hypothetical prote
38	36	66.7	247	2 G81013	1-acyl-sn-glycerol
39	36	66.7	247	2 A81957	1-acylglycerol-3-p
40	36	66.7	250	2 A69843	hypothetical prote
41	36	66.7	280	2 S61111	GPI2 protein - yea
42	36	66.7	292	2 A83779	hypothetical prote
43	36	66.7	351	2 D84541	hypothetical prote
44	36	66.7	385	2 S43540	YSD83 protein - ye
45	36	66.7	387	2 B90862	probable membrane

ALIGNMENTS

RESULT 1

C95307
probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) mag
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95307
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Welle, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95307
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-441 <KUR>
A;Cross-references: UNIPROT:Q92ZT6; GB:AE006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSyma
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: Sma0684
A;Genome: plasmid
C;Superfamily: L-lysine transport protein

Query Match 77.8%; Score 42; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIIW 7
|||:|
Db 92 GYWISIW 98

RESULT 2

T42216
multidrug resistance-associated protein homolog MLP-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42216
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.
Mol. Pharmacol. 53, 1068-1075, 1998
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins mai
A;Reference number: Z22081; MUID:98279126; PMID:9614210
A;Accession: T42216
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-1502 <HIR>
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3242457
A;Experimental source: strain Sprague-Dawley; liver
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 77.8%; Score 42; DB 2; Length 1502;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
| | | | : |
Db 964 GYWLSLW 970

RESULT 3
PC4117
replication protein homolog - Pyrococcus sp. (fragment)
N;Alternate names: hypothetical 391 protein
C;Species: Pyrococcus sp.
C;Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 17-May-1996
C;Accession: PC4117
R;Rashid, N.; Morikawa, M.; Imanaka, T.
Gene 166, 139-143, 1995
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.
A;Reference number: JC4514; MUID:96105215; PMID:8529878
A;Accession: PC4117
A;Molecule type: DNA
A;Residues: 1-391 <RAS>
A;Cross-references: DDBJ:D50018

Query Match 75.9%; Score 41; DB 2; Length 391;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YWLTIWG 8
| | | | |
Db 155 YWLTEWG 161

RESULT 4
E90446
permease [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90446
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <KUR>
A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G
C;Genetics:
A;Gene: SSO2718

Query Match 75.9%; Score 41; DB 2; Length 419;
Best Local Similarity 62.5%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
| : | | : |
Db 365 GFWETLWG 372

RESULT 5
C34903
Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C;Accession: C34903
R;Bedzyk, W.D.; Herron, J.N.; Edmondson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-react
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-142 <BED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 40; DB 2; Length 142;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
| | | | |
Db 126 GYWFAYWG 133

RESULT 6
B71038
probable Na+/H+-exchanging protein - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: B71038
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71038
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-425 <KAW>
A;Cross-references: UNIPROT:O59255; GB:AP000006; NID:g3236133; PIDN:BAA30706.1; PID:g3258
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1594

Query Match 74.1%; Score 40; DB 2; Length 425;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
| | | | |
Db 319 GAWLTAWG 326

RESULT 7
C95282
probable ABC transporter, periplasmic solute-binding protein, family 5 Sma0302 [imported]
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: C95282
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95282
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-508 <KUR>
A;Cross-references: UNIPROT:Q930N2; GB:AE006469; PIDN:AAK64821.1; PID:g14523232; GSPDB:G
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation

Query Match 74.1%; Score 40; DB 2; Length 508;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
AF1978
hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF1978
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF1978
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <KUR>
A;Cross-references: UNIPROT:Q8YX40; GB:BA000019; PIDN:BA073334.1; PID:g17130724; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1377

```

Query Match      72.2%; Score 39; DB 2; Length 376;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 9
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C:Species: Lactobacillus sakei
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T46745
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, J. Bacteriol. 180, 4154-4159, 1998
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of A:Reference number: Z23141; MUID:98361904; PMID:9696763
A:Accession: T46745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ZUN>
A:Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:g2764610
C:Genetics:
A:Gene: arcD
C:Function:
A:Description: necessary for arginine transport; involved in ornithine-arginine exchange
A:Pathway: arginine catabolism
C:Superfamily: L-lysine transport protein

Query Match	72.2%;	Score 39;	DB 2;	Length 475;
Best Local Similarity	71.4%;	Pred. No. 99;		

	Matches	5; Conservative	1; Mismatches	1; Indels	0; Gaps	0;
Qy	1	GYWLTIW	7			
		:				
Dp	94	GYWLSAW	100			

RESULT 10
C86879
arginine/ornitine antiporter [imported] - *Lactococcus lactis* subsp. *lactis* (strain
C; Species: *Lactococcus lactis* subsp. *lactis*
C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C; Accession: C86879
R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.;
Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium *Lactococcus*
A; Reference number: AB6625; MUID:21235186; PMID:11337471
A; Accession: C86879
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-490 <STO>
A; Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:gl2725084; PIDN:AAK06133.1
A; Experimental source: strain IL1403
C; Genetics:
A; Gene: arcD1
C; Superfamily: L-lysine transport protein

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Query Match      72.2%; Score 39; DB 2; Length 490;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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RESULT 11
T35739
probable integral membrane protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T35739
R/Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajan
submitted to the EMBL Data Library, August 1999
A/Reference number: Z21588
A/Accession: T35739
A/Status: preliminary; translated from GB/EMBL/DBSJ
A/Molecule type: DNA
A/Residues: 1-118 <SAU>
A/Cross-references: UNIPROT:Q9S2K9; EMBL:AL109732; PIDN:CAB52050.1; GSPDB:GN0007
A/Experimental source: strain A3 (2)
C/Genetics:
A/Gene: SCOEDB:SC7H2.08
C/Superfamily: Streptomyces coelicolor probable integral membrane protein SC7H2

Query Match	70.4%	Score 38;	DB 2;	Length 118;
Best Local Similarity	57.1%	Pred. No. 38;		
Matches 4:	Conservative	3;	Mismatches	0;
			Indels	0;
			Gaps	0;

RESULT 12
C75176
na+/h+ antiporter (napa-2) PAB0390 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C75176
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosomes

A;Reference number: A75001
A;Accession: C75176
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <KAW>
A;Cross-references: UNIPROT:Q9V160; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4949
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: napA-2; PAB0390
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match 70.4%; Score 38; DB 2; Length 426;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
|:|:|
Db 320 GAWITAWG 327

RESULT 13
G90251
ABCTransporter [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: G90251
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <KUR>
A;Cross-references: UNIPROT:Q97ZC3; GB:AE006641; NID:g13814184; PIDN:AAK41270.1; GSPDB:G
C;Genetics:
A;Gene: SSO0999

Query Match 70.4%; Score 38; DB 2; Length 477;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WLTIWG 8
|:|:|
Db 415 WITVWG 420

RESULT 14
T50103
probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T50103
R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 2000
A;Reference number: Z25038
A;Accession: T50103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-583 <SEE>
A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN00066; SPDB:
A;Experimental source: strain 972h(-); cosmid c1783
C;Genetics:
A;Gene: SPDB:SPAC1783.01
A;Map position: 1

Query Match 70.4%; Score 38; DB 2; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8

Db 244 GRWPTIWG 251
|:|:|:|

RESULT 15
S58888
Ins P4-binding protein - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 04-Apr-2004
C;Accession: S58888
R;Cullen, P.J.; Hsuan, J.J.; Truong, O.; Letcher, A.J.; Jackson, T.R.; Dawson, A.P.; Irv
Nature 376, 527-530, 1995
A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the
A;Reference number: S58888; MUID:95364929; PMID:7637787
A;Accession: S58888
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-829 <CUL>
A;Cross-references: EMBL:X89399
F;328-539/Domain: ras-specific GAP catalytic domain homology <GAP>
F;571-670/Domain: pleckstrin repeat homology <PLK>

Query Match 70.4%; Score 38; DB 2; Length 829;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
|:|:|:|
Db 689 GHWLCCWG 696

Search completed: January 3, 2005, 12:13:50
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 11:52:29 ; Search time 187 Seconds
(without alignments)
24.615 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywltiwg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	79.6	221	2 Q74JK6	Q74jk6 lactobacill
2	43	79.6	221	2 AAS08923	Aas08923 lactobaci
3	43	79.6	733	2 Q8H2N7	Q8h2n7 oryza sativ
4	42	77.8	284	2 Q6MC01	Q6mc01 parachlamyd
5	42	77.8	284	2 CAF23898	Caf23898 parachlam
6	42	77.8	441	2 Q92ZT6	Q92zt6 rhizobium m
7	42	77.8	1308	2 Q8T6H2	Q8t6h2 dictyosteli
8	42	77.8	1498	1 MRP6_MOUSE	Q9rls7 mus musculu
9	42	77.8	1502	1 MRP6_RAT	Q88269 rattus norv
10	42	77.8	1503	1 MRP6_HUMAN	Q95255 homo sapien
11	41	75.9	266	2 Q82Z85	Q82z85 enterococcu
12	41	75.9	376	2 Q6CBE4	Q6cbe4 yarrowia li
13	41	75.9	413	2 Q9HKA9	Q9hka9 thermoplas
14	41	75.9	419	2 Q97VB7	Q97vb7 sulfolobus
15	41	75.9	736	2 Q8DMV4	Q8dmv4 synecococc
16	41	75.9	1052	2 Q7YZ84	Q7yz84 plasmodium
17	41	75.9	1652	2 Q74DR3	Q74dr3 geobacter s
18	41	75.9	1652	2 AAR34628	Aar34628 geobacter
19	40	74.1	167	1 OB_MACMU	Q28504 macaca mula
20	40	74.1	331	2 Q775C7	Q775c7 bordetella
21	40	74.1	331	2 AAR97683	Aar97683 bordetell
22	40	74.1	401	2 Q9KHQ6	Q9khg6 bacteroides
23	40	74.1	425	2 O59255	O59255 pyrococcus
24	40	74.1	508	2 Q930N2	Q930n2 rhizobium m
25	40	74.1	1970	2 Q88H71	Q88h71 pseudomonas
26	39	72.2	91	2 Q82A22	Q82a22 streptomyce
27	39	72.2	117	2 Q7S013	Q7s013 neurospora
28	39	72.2	144	2 Q6M566	Q6m566 corynebacte
29	39	72.2	144	2 CAF21531	Caf21531 corynebac
30	39	72.2	162	2 Q8NQB6	Q8nqb6 corynebacte
31	39	72.2	253	2 Q32816	Q32816 lactococcus

32	39	72.2	257	2 Q9ARZ0	Q9arz0 oryza sativ
33	39	72.2	312	2 Q6C129	Q6c129 yarrowia li
34	39	72.2	376	2 Q8YX40	Q8yx40 anabaena sp
35	39	72.2	432	2 Q8ZUS8	Q8zus8 pyrobaculum
36	39	72.2	443	2 Q7NSJ2	Q7nsj2 chromobacte
37	39	72.2	459	2 Q9KGV3	Q9kgv3 lactococcus
38	39	72.2	469	2 Q6TK71	Q6tk71 streptococc
39	39	72.2	469	2 AAR30325	Aar30325 streptoco
40	39	72.2	471	2 Q6HP27	Q6hp27 bacillus th
41	39	72.2	471	2 Q73E85	Q73e85 bacillus ce
42	39	72.2	471	2 Q81IH9	Q81ih9 bacillus ce
43	39	72.2	471	2 AAS39409	Aas39409 bacillus
44	39	72.2	475	1 ARCD_LACSK	O53092 lactobacill
45	39	72.2	475	2 Q8DWP9	Q8dwp9 streptococc

ALIGNMENTS

RESULT 1

Q74JK6 PRELIMINARY; PRT; 221 AA.
AC Q74JK6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN OrderedLocusNames=LJ1101;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwhlien M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1; -.
DR InterPro; IPR004254; HlyIII-related.
DR InterPro; IPR005744; HlyIII.
DR Pfam; PF03006; HlyIII; 1.
DR TIGRFAMs; TIGR01065; hlyIII; 1.
KW Complete proteome.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 70;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8

Db 172 GFWLLVWG 179
|:|:|:|

RESULT 2

AAS08923 PRELIMINARY; PRT; 221 AA.
ID AAS08923
AC AAS08923;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN LJ1101.
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL: AE017203; AAS08923.1; -.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
Db 172 GFWLLVWG 179

RESULT 3
Q8H2N7 PRELIMINARY; PRT; 733 AA.
ID Q8H2N7
AC Q8H2N7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OJ1138_B05.118.
GN Name=OJ1138_B05.118;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP005486; BAC16197.1; -.
DR Gramene; Q8H2N7; -.
DR InterPro; IPR007658; DUF594.
DR Pfam; PF04578; DUF594; 1.
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;

Query Match 79.6%; Score 43; DB 2; Length 733;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWLTIWG 8
Db 328 YWTTIWG 334

RESULT 4
Q6MC01 PRELIMINARY; PRT; 284 AA.
ID Q6MC01
AC Q6MC01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=pc1174;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=null;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA Rattei T., Mewes H.-W., Wagner M.;
SQ SEQUENCE FROM N.A.
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RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL: BX908798; CAF23898.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;

Query Match 77.8%; Score 42; DB 2; Length 284;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLTIWG 8
Db 273 YWLSLWG 279

RESULT 5
CAF23898 PRELIMINARY; PRT; 284 AA.
ID CAF23898
AC CAF23898;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN PC1174.
OS Parachlamydia sp. UWE25.
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UWE25;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA Rattei T., Mewes H., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UWE25;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,
RA Rattei T., Mewes H., Wagner M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX908798; CAF23898.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;

Query Match 77.8%; Score 42; DB 2; Length 284;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLTIWG 8
Db 273 YWLSLWG 279

RESULT 6
Q92ZT6 PRELIMINARY; PRT; 441 AA.
ID Q92ZT6
AC Q92ZT6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable transport protein.
GN OrderedLocusNames=RA0363; ORFNames=Sma0684;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSymA megaplasmid.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21368234; PubMed=11474104;
RA Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P.,
RA Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B.,
RA Ramsperger U., Surzycki R., Thebault P., Vandenbol M.,
RA Vorhoeelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT "The composite genome of the legume symbiont Sinorhizobium meliloti.";
RL Science 293:668-672(2001).
DR EMBL; AE007228; AAK65021.1; -.
DR PIR; C95307; C95307.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Plasmid; Transmembrane; Transport.
SQ SEQUENCE 441 AA; 46277 MW; B6F5C9EC96011AD0 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 441;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 92 GYWISIW 98
|||:|

RESULT 7
Q8T6H2
ID Q8T6H2 PRELIMINARY; PRT; 1308 AA.
AC Q8T6H2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ABC transporter ABCC.7.
GN Name=abcC7;
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ax4;
RA Anjard C., Loomis W.F.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AF474339; AAL85710.1; -.
DR HSSP; P08716; 1MT0.
DR DictyBase; DDB0201630; abcC7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS50929; ABC_TM1F; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW ATP-binding.
SQ SEQUENCE 1308 AA; 149576 MW; 336120AC8F737AC1 CRC64;

Query Match 77.8%; Score 42; DB 2; Length 1308;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLTIIW 7
Db 764 YWLTIIW 769
|||||

RESULT 8
MRP6_MOUSE
ID MRP6_MOUSE STANDARD; PRT; 1498 AA.
AC Q9RJ57; Q80YB6;
DT 01-OCT-2004 (Rel. 45, Created)
DT 01-OCT-2004 (Rel. 45, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6).
GN Name=Abcc6; Synonyms=Mrp6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ddy; TISSUE=Liver;
RA Morikawa A., Suzuki H., Hirohashi T., Sugiyama Y.;
RT "Mus musculus mRNA for multidrug resistance-associated protein 6 (MRP6), complete cds.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 685-1498 FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP REVIEW.
RX DOI=10.1038/mp.a002623.01;
RA Beck C., Le Saux O., Varadi A., Boyd C.;
RT "Abcc6.";
RL (er) AfCS-Nature Molecule Pages (2004).


```
CC -!- FUNCTION: May participate directly in the active transport of
CC drugs into subcellular organelles or influence drug distribution
CC indirectly (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC -----
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CC -----
CC EMBL; AB028737; BAA83820.1; -.
CC EMBL; BC049980; AAH49980.1; -.
CC HSSP; Q03518; 1JJ7.
CC MGD; MGI:1351634; Abcc6.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_transporter.
CC InterPro; IPR005292; MRP_assoc.
CC Pfam; PF00664; ABC_membrane; 2.
CC Pfam; PF00005; ABC_tran; 2.
CC ProDom; PD000006; ABC_transporter; 1.
CC SMART; SM00382; AAA; 2.
CC TIGRFAMs; TIGR00957; MRP_assoc_pro; 1.
CC PROSITE; PS0929; ABC_TM1F; 2.
CC PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
CC PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
CC ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.
KW DOMAIN 1 37 Extracellular (By similarity).
FT TRANSMEM 38 58 Extracellular (By similarity).
FT DOMAIN 59 78 Cytoplasmic (By similarity).
FT TRANSMEM 79 99 Cytoplasmic (By similarity).
FT DOMAIN 100 104 Extracellular (By similarity).
FT TRANSMEM 105 125 Extracellular (By similarity).
FT DOMAIN 126 137 Cytoplasmic (By similarity).
FT TRANSMEM 138 155 Extracellular (By similarity).
FT DOMAIN 156 173 Extracellular (By similarity).
FT TRANSMEM 174 194 Extracellular (By similarity).
FT DOMAIN 195 300 Cytoplasmic (By similarity).
FT TRANSMEM 301 321 Cytoplasmic (By similarity).
FT DOMAIN 322 347 Extracellular (By similarity).
FT TRANSMEM 348 368 Extracellular (By similarity).
FT DOMAIN 369 424 Cytoplasmic (By similarity).
FT TRANSMEM 425 445 Extracellular (By similarity).
FT DOMAIN 446 448 Extracellular (By similarity).
FT TRANSMEM 449 469 Extracellular (By similarity).
FT DOMAIN 470 531 Cytoplasmic (By similarity).
FT TRANSMEM 532 552 Extracellular (By similarity).
FT DOMAIN 553 574 Extracellular (By similarity).
FT TRANSMEM 575 595 Extracellular (By similarity).
FT DOMAIN 596 934 Cytoplasmic (By similarity).
FT TRANSMEM 935 955 Extracellular (By similarity).
FT DOMAIN 956 992 Extracellular (By similarity).
FT TRANSMEM 993 1013 Cytoplasmic (By similarity).
FT DOMAIN 1014 1056 Cytoplasmic (By similarity).
FT TRANSMEM 1057 1077 Extracellular (By similarity).
FT DOMAIN 1078 1099 Extracellular (By similarity).
FT TRANSMEM 1099 1170 Cytoplasmic (By similarity).
FT DOMAIN 1170 1170 Cytoplasmic (By similarity).
FT TRANSMEM 1171 1191 Extracellular (By similarity).
FT DOMAIN 1192 1193 Extracellular (By similarity).
FT TRANSMEM 1194 1214 Cytoplasmic (By similarity).
FT DOMAIN 1215 1498 Cytoplasmic (By similarity).
FT TRANSMEM 1498 1591 ABC transporter 1.
FT DOMAIN 1591 1694 ABC transporter 2.
FT NP_BIND 1694 1706 ATP (Potential).
FT NP_BIND 1706 1706 ATP (Potential).
FT CARBOHYD 1706 1706 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 1706 1706 N-linked (GlcNAc. .) (Potential).
FT CONFLICT 1706 1706 A -> V (in Ref. 2).
```

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FT CONFLICT 927 927 I -> T (in Ref. 2).
FT CONFLICT 1401 1401 H -> Q (in Ref. 2).
FT CONFLICT 1448 1448 L -> V (in Ref. 2).
FT CONFLICT 1477 1477 N -> S (in Ref. 2).
SQ SEQUENCE 1498 AA; 164788 MW; EFCFF33F0EEC813C CRC64;

Query Match 77.8%; Score 42; DB 1; Length 1498;
Best Local Similarity 71.4%; Pred. No. 5.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
Db 960 GYWLSLW 966

RESULT 9
MRP6 RAT
ID_MRP6_RAT STANDARD; PRT; 1502 AA.
AC O88269;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-
DE family C, member 6) (MRP-like protein-1) (MLP-1).
GN Name=Abcc6; Synonyms=Mrp6, Mpl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=98279126; PubMed=9614210;
RA Hirohashi T., Suzuki H., Ito K., Ogawa K., Kume K., Shimizu T.,
RA Sugiyama Y.;
RT "Hepatic expression of multidrug resistance-associated protein-like
RT proteins maintained in eisa hyperbilirubinemic rats.";
RL Mol. Pharmacol. 53:1068-1075(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=20159081; PubMed=10692506;
RA Madon J., Hagenbuch B., Landmann L., Meier P.J., Stieger B.;
RT "Transport function and hepatocellular localization of mrp6 in rat
RT liver.";
RL Mol. Pharmacol. 57:634-641(2000).
CC -!- FUNCTION: May participate directly in the active transport of
CC drugs into subcellular organelles or influence drug distribution
CC indirectly (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: High in liver and lower in duodenum and
CC kidney.
CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.
CC -----
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CC -----
CC EMBL; AB010466; BAA28954.1; -.
CC EMBL; U73038; AAD12747.1; -.
CC PIR; T42216; T42216.
CC HSSP; P08716; 1MT0.
CC RGD; 620268; Abcc6.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR001140; ABC_TM_transpt.
CC InterPro; IPR003439; ABC_transporter.
CC InterPro; IPR005292; MRP_assoc.
CC Pfam; PF00664; ABC_membrane; 2.
CC Pfam; PF00005; ABC_tran; 2.
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DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMs; TIGR00957; MRP_assoc_pro; 1.
DR PROSITE; PS0929; ABC_TMIF; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS0893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.
FT DOMAIN 5 37 Extracellular (By similarity).
FT TRANSMEM 38 58 1 (By similarity).
FT DOMAIN 59 78 Cytoplasmic (By similarity).
FT TRANSMEM 79 99 2 (By similarity).
FT DOMAIN 100 104 Extracellular (By similarity).
FT TRANSMEM 105 125 3 (By similarity).
FT DOMAIN 126 137 Cytoplasmic (By similarity).
FT TRANSMEM 138 155 4 (By similarity).
FT DOMAIN 156 173 Extracellular (By similarity).
FT TRANSMEM 174 194 5 (By similarity).
FT DOMAIN 195 300 Cytoplasmic (By similarity).
FT TRANSMEM 301 321 6 (By similarity).
FT DOMAIN 322 347 Extracellular (By similarity).
FT TRANSMEM 348 368 7 (By similarity).
FT DOMAIN 369 424 Cytoplasmic (By similarity).
FT TRANSMEM 425 445 8 (By similarity).
FT DOMAIN 446 448 Extracellular (By similarity).
FT TRANSMEM 449 469 9 (By similarity).
FT DOMAIN 470 531 Cytoplasmic (By similarity).
FT TRANSMEM 532 552 10 (By similarity).
FT DOMAIN 553 574 Extracellular (By similarity).
FT TRANSMEM 575 595 11 (By similarity).
FT DOMAIN 596 938 Cytoplasmic (By similarity).
FT TRANSMEM 939 959 12 (By similarity).
FT DOMAIN 960 996 Extracellular (By similarity).
FT TRANSMEM 997 1017 13 (By similarity).
FT DOMAIN 1018 1060 Cytoplasmic (By similarity).
FT TRANSMEM 1061 1081 14 (By similarity).
FT DOMAIN 1082 1082 Extracellular (By similarity).
FT TRANSMEM 1083 1103 15 (By similarity).
FT DOMAIN 1104 1174 Cytoplasmic (By similarity).
FT TRANSMEM 1175 1195 16 (By similarity).
FT DOMAIN 1196 1197 Extracellular (By similarity).
FT TRANSMEM 1198 1218 17 (By similarity).
FT DOMAIN 1219 1502 Cytoplasmic (By similarity).
FT TRANSMEM 1267 851 ABC transporter 1.
FT DOMAIN 1264 1498 ABC transporter 2.
FT NP_BIND 661 668 ATP (Potential).
FT NP_BIND 1298 1305 ATP (Potential).
FT CARBOHYD 21 21 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1502 AA; 164995 MW; 539901B6747A28 CRC64;

Query Match 77.8%; Score 42; DB 1; Length 1502;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYWLTIW 7
DQ 964 GYWLTLW 970

RESULT 10
MRP6_HUMAN
ID MRP6_HUMAN STANDARD; PRT; 1503 AA.
AC O95255; P78420; Q9UMZ7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6) (Anthracycline resistance-associated protein)
DE (Multi-specific organic anion transporter-E) (MOAT-E).
GN Name=ABCC6; Synonyms=MRP6, ARA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99107222; PubMed=98922204;
RA Kool M., van der Linden M., de Haas M., Baas F., Borst P.;
RT "Expression of human MRP6, a homologue of the multidrug resistance protein gene MRP1, in tissues and cancer cells.";
RL Cancer Res. 59:175-182(1999).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99425270; PubMed=10493829;
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
RT "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
RL Genomics 60:295-308(1999).
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=99352020; PubMed=10424734;
RA Belinsky M.G., Kruh G.D.;
RT "MOAT-E (ARA) is a full-length MRP/cMOAT subfamily transporter expressed in kidney and liver.";
RL Br. J. Cancer 80:1342-1349(1999).
RN
RP FUNCTION, AND CHARACTERIZATION OF VARIANTS PXE PHE-1298; ARG-1302 AND SER-1321.
RX MEDLINE=21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200;
RA Ilias A., Urban Z., Seidl T.L., Le Saux O., Sinko E., Boyd C.D., Sarkadi B., Varadi A.;
RT "Loss of ATP-dependent transport activity in pseudoxanthoma elasticum-associated mutants of human ABCC6 (MRP6).";
RL J. Biol. Chem. 277:16860-16867(2002).
RN
RP REVIEW, AND VARIANT PXE PRO-455.
RX MEDLINE=21321623; PubMed=11427982; DOI=10.1016/S1471-4914(00)01869-4;
RA Uitto J., Pulkkinen L., Ringpfeil F.;
RT "Molecular Genetics of pseudoxanthoma elasticum: a metabolic disorder at the environment-genome interface?";
RL Trends Mol. Med. 7:13-17(2001).
RN
RP VARIANT GLN-1268.
RX MEDLINE=20374463; PubMed=10913334; DOI=10.1006/bbrc.2000.3101;
RA Germain D.P., Perdu J., Remones V., Jeunemaitre X.;
RT "Homozygosity for the R1268Q mutation in MRP6, the pseudoxanthoma elasticum gene, is not disease-causing.";
RL Biochem. Biophys. Res. Commun. 274:297-301(2000).
RN
RP VARIANT ARG-64.
RX MEDLINE=20514578; PubMed=11058917;
RX DOI=10.1002/1098-1004(200011)16:5<449::AID-HUMU24>3.0.CO;2-O;
RA Germain D.P., Perdu J., Remones V., Manzoni K., Jeunemaitre X.;
RT "Identification of two polymorphisms (c189G>C; c190T>C) in exon 2 of the human MRP6 gene (ABCC6) by screening of pseudoxanthoma elasticum patients: possible sequence correction?";
RL Hum. Mutat. 16:449-449(2000).
RN
RP VARIANT PXE CYS-1339, AND VARIANT GLN-632.
RX MEDLINE=20408303; PubMed=10954200;
RA Struk B., Cai L., Zaech S., Ji W., Chung J., Lumsden A., Stumm M., Huber M., Schaen L., Kim C.-A., Goldsmith L.A., Viljoen D., Figuera L.E., Fuchs W., Munier F., Ramesar R., Hohl D., Richards R., Neldner K.H., Lindpaintner K.;
RT "Mutations of the gene encoding the transmembrane transporter protein ABC-C6 cause pseudoxanthoma elasticum.";
RL J. Mol. Med. 78:282-286(2000).
RN
RP VARIANTS PXE PRO-1114; GLN-1138 AND TRP-1314, AND VARIANT ALA-614.
RX MEDLINE=20296630; PubMed=10835642; DOI=10.1038/76102;
RA Le Saux O., Urban Z., Tschuch C., Csiazar K., Bacchelli B., Quaglini D., Pasquali-Ronchetti I., Pope F.M., Richards A., Terry S., Bercovitch L., de Paepe A., Boyd C.D.;
RT "Mutations in a gene encoding an ABC transporter cause pseudoxanthoma

RT elasticum.";

RL Nat. Genet. 25:223-227(2000).

RN [10]

RP VARIANT PXE TRP-1138, AND VARIANT GLN-1268.

RX MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297;

RA Ringpfeil F., Lebowhl M.G., Cristiano A.M., Uitto J.;

RT "Pseudoxanthoma elasticum: mutations in the MRP6 gene encoding a

RT transmembrane ATP-binding cassette (ABC) transporter.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).

RN [11]

RP VARIANTS PXE LYS-411; GLN-518; SER-568; PRO-673; GLN-765; PRO-1114;

RP TRP-1121; PRO-1138; GLN-1138; ASP-1203; PHE-1298; ILE-1301; ARG-1302;

RP PRO-1303; GLN-1314; TRP-1314; SER-1321; CYS-1339; HIS-1347; ASN-1361

RP AND THR-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-319;

RP LYS-497; ALA-614; GLN-632; HIS-953; CYS-1241 AND GLN-1268.

RX MEDLINE=21426347; PubMed=11536079;

RA Le Saux O., Beck K., Sachsinger C., Silvestri C., Treiber C.,

RA Goering H.H.H., Johnson E.W., De Faepe A., Pope F.M.,

RA Pasquali-Ronchetti I., Bercovitch L., Terry S., Boyd C.D.;

RT "A spectrum of ABCC6 mutations is responsible for pseudoxanthoma

RT elasticum.";

RL Am. J. Hum. Genet. 69:749-764(2001).

RN [12]

RP VARIANTS PXE 60-ARG--TYR-62 DEL; ARG-364 AND ARG-1354, AND VARIANT

RP GLY-265.

RX MEDLINE=21558431; PubMed=11702217; DOI=10.1007/s004390100582;

RA Pulkkinen L., Nakano A., Ringpfeil F., Uitto J.;

RT "Identification of ABCC6 pseudogenes on human chromosome 16p:

RT implications for mutation detection in pseudoxanthoma elasticum.";

RL Hum. Genet. 109:356-365(2001).

RN [13]

RP VARIANTS ALA-614; GLN-632 AND GLN-1268.

RX MEDLINE=21632106; PubMed=11776382;

RA Wang J., Near S., Young K., Connelly P.W., Hegele R.A.;

RT "ABCC6 gene polymorphism associated with variation in plasma

RT lipoproteins.";

RL J. Hum. Genet. 46:699-705(2001).

CC -!- FUNCTION: May participate directly in the active transport of

CC drugs into subcellular organelles or influence drug distribution

CC indirectly. Transports glutathione conjugates as leukotriene-c4

CC and LTC4) and N-ethylmaleimide S-glutathione (NEM-GS).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed in kidney and liver. Very low

CC expression in other tissues.

CC -!- DISEASE: Defects in ABCC6 are a cause of autosomal dominant

CC pseudoxanthoma elasticum (AD-PXE) [MIM:177850]. PXE is a disorder

CC characterized by calcification of elastic fibers in skin, arteries

CC and retina that results in dermal lesions with associated laxity

CC and loss of elasticity, arterial insufficiency and retinal

CC hemorrhages leading to macular degeneration.

CC -!- DISEASE: Defects in ABCC6 are a cause of autosomal recessive

CC pseudoxanthoma elasticum (AR-PXE) [MIM:264800].

CC -!- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.

CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous

CC gene model prediction.

CC -!- DATABASE: NAME=Mutations of the ABCC6 gene;

CC NOTE=Retina International's Scientific Newsletter;

CC WWW="http://www.retina-international.com/sci-news/abcc6mut.htm".

CC -----

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CC -----

DR EMBL; AF076622; AAC79696.1; --.

DR EMBL; U91318; AAC15785.1; ALT_SEQ.

DR EMBL; AF168791; AAD51293.1; --.

DR HSSP; P08716; 1MT0.

DR Genew; HGNC:57; ABCC6.

DR MIM; 603234; --.

DR MIM; 177850; --.

DR MIM; 264800; --.

DR GO; GO:0005624; C:membrane fraction; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0005524; F:ATP binding; TAS.

DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; TAS.

DR GO; GO:0005215; F:transporter activity; TAS.

DR GO; GO:0042493; P:response to drug; TAS.

DR GO; GO:0006810; P:transport; TAS.

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR001140; ABC_TM_transpt.

DR InterPro; IPR003439; ABC_transporter.

DR InterPro; IPR005292; MRP_assoc.

DR Pfam; PF00664; ABC_membrane; 2.

DR Pfam; PF00005; ABC_tran; 2.

DR ProDom; PD000006; ABC_transporter; 1.

DR SMART; SM00382; AAA; 2.

DR TIGRFAMS; TIGR00957; MRP_assoc_pro; 1.

DR PROSITE; PS50929; ABC_TM1F; 2.

DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.

DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.

KW ATP-binding; Disease mutation; Glycoprotein; Polymorphism; Repeat;

KW Transmembrane; Transport; Vision.

FT DOMAIN 1 31 Extracellular (By similarity).

FT TRANSMEM 32 52 1 (By similarity).

FT DOMAIN 53 72 Cytoplasmic (By similarity).

FT TRANSMEM 73 93 2 (By similarity).

FT DOMAIN 94 98 Extracellular (By similarity).

FT TRANSMEM 99 119 3 (By similarity).

FT DOMAIN 120 131 Cytoplasmic (By similarity).

FT TRANSMEM 132 149 4 (By similarity).

FT DOMAIN 150 167 Extracellular (By similarity).

FT TRANSMEM 168 188 5 (By similarity).

FT DOMAIN 189 302 Cytoplasmic (By similarity).

FT TRANSMEM 303 323 6 (By similarity).

FT DOMAIN 324 349 Extracellular (By similarity).

FT TRANSMEM 350 370 7 (By similarity).

FT DOMAIN 371 426 Cytoplasmic (By similarity).

FT TRANSMEM 427 447 8 (By similarity).

FT DOMAIN 448 450 Extracellular (By similarity).

FT TRANSMEM 451 471 9 (By similarity).

Query Match 77.8%; Score 42; DB 1; Length 1503;

Best Local Similarity 71.4%; Pred. No. 6e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWLTIW 7

Db 965 GYWLSLW 971

RESULT 11

Q82Z85

ID Q82Z85 PRELIMINARY; PRT; 266 AA.

AC Q82Z85;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN OrderedLocusNames=EF3185;

OS Enterococcus faecalis (Streptococcus faecalis).

OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OX NCBI_TaxID=1351;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=V583 / ATCC 700802;

RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;

RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,

RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,

RA Daugherty S.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,

RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,

RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,

RA Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RL Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AE016957; AAO82859.1; -.
DR TIGR; EF3185; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 266 AA; 28291 MW; CD6E72C4DF555A36 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 266;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
Db 203 GTWITLWG 210

RESULT 12
Q6CBE4 PRELIMINARY; PRT; 376 AA.
AC Q6CBE4;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P38071 Saccharomyces cerevisiae YBR026c.
GN ORFNames=YAL10C19624g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boismare A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382129; CAG82338.1; -.
SQ SEQUENCE 376 AA; 41206 MW; E085FF7C32379DCB CRC64;

Query Match 75.9%; Score 41; DB 2; Length 376;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
Db 301 GYWLTRW 307

RESULT 13
Q9HKA9
ID Q9HKA9 PRELIMINARY; PRT; 413 AA.
AC Q9HKA9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transport protein related protein.
GN OrderedLocusNames=Ta0692;
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL; AL445065; CAC11830.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 413 AA; 45192 MW; 307093BC358063D4 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 413;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIWG 8
Db 354 GFWETLWG 361

RESULT 14
Q97VB7
ID Q97VB7 PRELIMINARY; PRT; 419 AA.
AC Q97VB7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Permease.
GN OrderedLocusNames=SS02718;
OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35092 / DSM 1617 / P2;
RX MEDLINE=21332296; PubMed=11427726;
RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMBL; AE006865; AAK42828.1; -.
DR PIR; E90446; E90446.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR Pfam; PF00083; Sugar tr; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome.
SQ SEQUENCE 419 AA; 46499 MW; 6DB6AB6B5C6DA267 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 419;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 8
|:| |:|
Db 365 GFWETLWG 372

RESULT 15
Q8DMV4
ID Q8DMV4 PRELIMINARY; PRT; 736 AA.
AC Q8DMV4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cellulose synthase.
GN OrderedLocusNames=tl10007;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; AP005369; BAC07560.1; -.
DR InterPro; IPR001173; Glyco_trans_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Complete proteome.
SQ SEQUENCE 736 AA; 85049 MW; D31C506166FD9624 CRC64;

Query Match 75.9%; Score 41; DB 2; Length 736;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
||| ||
Db 557 GYWLHIW 563

Search completed: January 3, 2005, 12:13:06
Job time : 190 secs

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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:13:55 ; Search time 148 Seconds
(without alignments)
19.391 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywlting 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 153769

Minimum DB seq length: 0
Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	61.1	7	5 ABP53964	Abp53964 VEGFR-3 b
2	33	61.1	8	5 ABP53965	Abp53965 VEGFR-3 b
3	32	59.3	7	3 AAY76794	Aay76794 Somatosta
4	32	59.3	7	5 ABP53418	Abp53418 Backbone
5	31	57.4	8	2 AAW97529	Aaw97529 Antigenic
6	29	53.7	5	2 AAR29452	Aar29452 Endotheli
7	29	53.7	5	2 AAR69224	Aar69224 Endotheli
8	29	53.7	5	2 AAW56531	Aaw56531 Antigenic
9	29	53.7	7	8 ADJ25834	Adj25834 Tyrosine
10	29	53.7	8	4 ABP22594	Abp22594 HIV A11 m
11	29	53.7	8	4 ABP14287	Abp14287 HIV A03 s
12	29	53.7	8	4 ABP18686	Abp18686 HIV B62 s
13	29	53.7	8	4 ABP20292	Abp20292 HIV A03 m
14	29	53.7	8	4 ABP19992	Abp19992 HIV A03 m
15	29	53.7	8	4 ABP12050	Abp12050 HIV A02 s
16	29	53.7	8	4 ABP14288	Abp14288 HIV A03 s
17	29	53.7	8	4 ABP16999	Abp16999 HIV B27 s
18	29	53.7	8	4 ABP22402	Abp22402 HIV A11 m
19	29	53.7	8	7 ADL17320	Adl17320 DENSIN-18
20	29	53.7	8	8 ADH62133	Adh62133 Cyclic an
21	29	53.7	8	8 ADH62029	Adh62029 Cyclic an
22	29	53.7	8	8 ADH62062	Adh62062 Cyclic an
23	29	53.7	8	8 ADP67844	Adp67844 Anti-micr
24	29	53.7	8	8 ADP67877	Adp67877 Anti-micr
25	29	53.7	8	8 ADP67948	Adp67948 Anti-micr

26	29	53.7	8	8 ADQ28160	Adq28160 Excluded
27	29	53.7	8	8 ADQ28097	Adq28097 Excluded
28	29	53.7	8	8 ADQ28067	Adq28067 Excluded
29	28	51.9	6	2 AAR20438	Aar20438 Anti-b-en
30	28	51.9	6	2 AAR93713	Aar93713 Cyclo(-Ty
31	28	51.9	8	5 ADE03142	Ade03142 Hybrid po
32	28	51.9	8	8 ADH62036	Adh62036 Cyclic an
33	28	51.9	8	8 ADH62037	Adh62037 Cyclic an
34	28	51.9	8	8 ADH62043	Adh62043 Cyclic an
35	28	51.9	8	8 ADH62038	Adh62038 Cyclic an
36	28	51.9	8	8 ADH62065	Adh62065 Cyclic an
37	28	51.9	8	8 ADP67852	Adp67852 Anti-micr
38	28	51.9	8	8 ADP67858	Adp67858 Anti-micr
39	28	51.9	8	8 ADP67880	Adp67880 Anti-micr
40	28	51.9	8	8 ADP67853	Adp67853 Anti-micr
41	28	51.9	8	8 ADP67851	Adp67851 Anti-micr
42	28	51.9	8	8 ADQ28080	Adq28080 Excluded
43	28	51.9	8	8 ADQ28074	Adq28074 Excluded
44	28	51.9	8	8 ADQ28099	Adq28099 Excluded
45	28	51.9	8	8 ADQ28073	Adq28073 Excluded

ALIGNMENTS

RESULT 1

ABP53964

ID ABP53964 standard; peptide; 7 AA.

XX

AC ABP53964;

XX

DT 09-JAN-2003 (first entry)

XX

DE VEGFR-3 binding peptide SEQ ID NO:67.

XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnery; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 4..6 /note= "X is any amino acid"

FT

XX WO200257299-A2.

 PN | XX || XX | XX | 25-JUL-2002. |
PD	XX	16-JAN-2002; 2002WO-IB0000099.
PF	XX	17-JAN-2001; 2001US-0262476P.
XX	XX	(LUDW-) LUDWIG INST CANCER RES.
XX	XX	(LICN) LICENTIA LTD.
PI	XX	Alitalo K, Koivunen E, Kubo H;
XX	XX	WPI; 2002-691521/74.
XX	XX	New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT	XX	diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT	XX	such as cancer and diseases of neovascularization.
XX	XX	Claim 21; Page 81; 149pp; English.
PS	XX	The present invention describes an isolated peptide (I) that binds to and
XX	XX	inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC	XX	have cytostatic, hepatotropic, antiinflammatory, hypotensive,
CC	XX	

CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 7 AA;

Query Match 61.1%; Score 33; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
||| |
Db 1 GYWXXXW 7

RESULT 2
ABP53965
ID ABP53965 standard; peptide; 8 AA.
XX
AC ABP53965;
XX
DT 09-JAN-2003 (first entry)
XX
DE VEGFR-3 binding peptide SEQ ID NO:68.
XX
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;
KW cystostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;
KW vulnerrary; cell surface receptor; cancer; neovascularisation;
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;
KW diabetes; PDGF; platelet derived growth factor.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 4..6 /note= "X is any amino acid"
FT FT /note= "any amino acid"
FT
XX
PN WO200257299-A2.
XX
PD 25-JUL-2002.
XX
PF 16-JAN-2002; 2002WO-IB000099.
XX
PR 17-JAN-2001; 2001US-0262476P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
XX
PI Alitalo K, Koivunen E, Kubo H;
XX
DR WPI; 2002-691521/74.
XX
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,
PT such as cancer and diseases of neovascularization.
XX
PS Claim 22; Page 81; 149pp; English.
XX
CC The present invention describes an isolated peptide (I) that binds to and
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,

CC antidiabetic and vulnerary activities, and can be used in gene therapy.
CC Compositions and methods from the present invention are useful for
CC diagnosing, evaluating and treating disorders mediated by the activity of
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,
CC liver, spleen, kidney, lymph node, small intestine, blood cells,
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,
CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,
CC chronic hepatitis, haemangiomas and diabetes. The present sequence
CC represents a specifically claimed VEGFR-3 binding peptide from the
CC present invention
XX
SQ Sequence 8 AA;

Query Match 61.1%; Score 33; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
||| |
Db 1 GYWXXXW 7

RESULT 3
AAY76794
ID AAY76794 standard; peptide; 7 AA.
XX
AC AAY76794;
XX
DT 20-APR-2000 (first entry)
XX
DE Somatostatin analogue peptide 3181.
XX
KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;
KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;
KW gastrointestinal disorder; inflammatory disease; pancreatitis;
KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;
KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;
KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3 /note= "D-form residue"
FT FT /note= "Trp-NH2"
FT
XX
PN WO9965508-A1.
XX
PD 23-DEC-1999.
XX
PF 15-JUN-1999; 99WO-IL000329.
XX
PR 19-JUN-1998; 98US-00100360.
PR 02-DEC-1998; 98US-00203389.
XX
PA (PEPT-) PEPTOR LTD.
XX
PI Hornik V, Afargan MM, Gellerman G;
XX
DR WPI; 2000-136888/12.
XX
PT Cyclized somatostatin analogs for inhibiting growth hormone secretion
PT from anterior pituitary and as antiproliferative agents for the treatment
PT of tumors.
XX
PS Example 11; Page 61; 82pp; English.
XX
CC This sequence represents a somatostatin analogue of the invention. The
CC invention relates to a backbone cyclised somatostatin analogue that has
CC one building unit containing a nitrogen atom of the peptide backbone
CC connected to a bridging group comprising an amide, thioether, thioester

CC or disulphide. At least one building unit is connected via a bridging
CC group to form a cyclic structure with a moiety selected from a second
CC building unit, side chain of or N-terminal amino acid residue. A
CC composition containing the analogue may be used for preventing disorders
CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-
CC associated complications, gastrointestinal disorders, inflammatory
CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical
CC pain. It may also be used for diagnosing cancer. The backbone cyclic
CC analogue is used for imaging the existence of metastases. Somatostatin
CC analogues can be used for the treatment of patients with hormone-secreting
CC and hormone-dependent tumours. They reduce diarrhoea through the
CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct
CC effect on intestinal secretion. Somatostatin analogues selective to type
CC 2 and 5 receptors may be used for treatment of non-insulin dependent
CC diabetes mellitus. They are useful for the prevention of atherosclerosis
CC and restenosis. The analogues are metabolically stable, selective in
CC their in-vivo activities and safe
XX
SQ Sequence 7 AA;

Query Match 59.3%; Score 32; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
||| |
Db 1 GYWKVCW 7

RESULT 4
ABP53418
ID ABP53418 standard; peptide; 7 AA.

XX ABP53418;

XX 19-NOV-2002 (first entry)

XX Backbone cyclised somatostatin analogue PTR 3181.

XX Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;
KW somatotropin release inhibiting factor; somatostatin receptor subtype;
KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;
KW antidiabetic; antiinflammatory; somatostatin receptor ligand;
KW atherosclerosis; autoimmune disease; diabetic-associated complication;
KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;
KW pancreatitis; post-surgical pain.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally modified with Fmoc
(fluorenylmethoxycarbonyl)"

FT Misc-difference 3

FT Modified-site 7 /note= "D form residue"

FT Modified-site 7 /note= "amidated"

XX US2002052315-A1.

PN 02-MAY-2002.

XX 13-DEC-2000; 2000US-00734583.

PR 19-JUN-1998; 98US-00100360.

PR 02-DEC-1998; 98US-00203389.

PR 15-JUN-1999; 99WO-IL000329.

XX (HORN/) HORNIK V.

PA (AFAR/) AFARGAN M M.

PA (GELL/) GELLERMAN G.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2002-681319/73.
XX New backbone cyclized somatostatin analogs are e.g. useful in the
PT treatment of atherosclerosis, autoimmune diseases and cancers.
PT
XX Example 12; Page 21; 30pp; English.

XX The present invention describes backbone cyclised somatostatin analogues
CC (I) that incorporates at least one building unit containing one nitrogen
CC atom of the peptide backbone connected to a bridging group (comprising an
CC amide, thioether, thioester or disulfide) where at least one building
CC unit is connected via the bridging group to form a cyclic structure with
CC a moiety selected from the group consisting of a second building unit,
CC the side chain of an amino acid residue of the sequence or the N-terminal
CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,
CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and
CC can be used as a somatostatin receptor ligand. (I) are useful in the
CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
CC associated complications, endocrine disorders, inflammation,
CC gastrointestinal disorders, pancreatitis, post-surgical pain, and
CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging
CC the existence of metastases, it being labeled with a detectable probe.
CC The present sequence represents a backbone cyclised somatostatin analogue
CC from the present invention
XX

SQ Sequence 7 AA;

Query Match 59.3%; Score 32; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWLTIW 7
||| |

Db 1 GYWKVCW 7

RESULT 5

AAW97529
ID AAW97529 standard; peptide; 8 AA.

XX AAW97529;

XX 19-MAY-1999 (first entry)

XX Antigenic site of HN protein loop beta-4L23.

XX Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;
KW virus epitope; attachment protein; vaccine; immunodominant epitope.

XX Measles virus.

XX WO9902695-A2.

XX 21-JAN-1999.

XX 08-JUL-1998; 98WO-NL000390.

XX 08-JUL-1997; 97EP-00202100.

XX (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX Langedijk JPM, Van Oirschot JT;

XX WPI; 1999-120896/10.

XX Isolated proteinaceous substance - comprising at least one virus epitope
PT derived from an attachment protein of a paramyxovirus.

XX Disclosure; Page 48; 63pp; English.

XX AAW97452-571 represent antigenic sites derived from the haemagglutinin-
CC neuraminidase (HN) protein of the paramyxoviridae. The specification

CC describes 3-D models identifying a proteinaceous substance comprising at
CC least one virus epitope derived from the attachment protein, which
CC corresponds to an antigenic site present on one of the loops of HN. The
CC antigenic sites can be used to produce vaccines, to detect the viruses,
CC and to select the immunodominant epitope
XX
SQ Sequence 8 AA;

Query Match 57.4%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWLT I 6
| | | | |
Db 4 YWLT I 8

RESULT 6
AAR29452
ID AAR29452 standard; peptide; 5 AA.
XX
AC AAR29452;
XX
DT 25-MAR-2003 (revised)
DT 13-APR-1993 (first entry)
XX
DE Endothelin antagonist peptide.
XX
KW Hypertension; myocardial infarction; congestive heart failure;
KW endotoxic shock; subarachnoid haemorrhage; asthma; arrhythmias;
KW acute renal failure; preeclampsia; diabetes; metabolic; endocrinological;
KW neurological; disorders.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Ac-D-Trp"
FT
XX WO9220706-A1.
XX
PD 26-NOV-1992.
XX
PF 24-APR-1992; 92WO-US003408.
XX
PR 16-MAY-1991; 91US-00701274.
PR 18-DEC-1991; 91US-00809746.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Cody Wl, Depue P, Doherty AM, Taylor MD;
XX WPI; 1992-415706/50.
DR
XX New peptide(s) used as endothelin antagonists - for treating
PT hypertension, metabolic and endocrine disorders, heart failure, diabetes,
PT asthma, neurological disorders, etc.
XX
PS Claim 5; Page 95; 116pp; English.
XX
CC The peptide is an endothelin antagonist useful in controlling
CC hypertension, myocardial infarction, congestive heart failure, endotoxic
CC shock, subarachnoid haemorrhage, asthma, arrhythmias, acute renal
CC failure, preeclampsia, diabetes and metabolic, endocrinological and
CC neurological disorders. Administration is oral parenteral or by
CC inhalation in doses of 0.01-20 (esp. 0.01-10) mg/kg/ day. It may be
CC prepared by conventional peptide synthesis. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 5 AA;

Query Match 53.7%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLT I W 7
| | | |
Db 1 WLD I W 5

RESULT 7
AAR69224
ID AAR69224 standard; peptide; 5 AA.
XX
AC AAR69224;
XX
DT 25-MAR-2003 (revised)
DT 06-MAR-1995 (first entry)
XX
DE Endothelin C-terminal peptide analog, useful as antagonist.
XX
KW Endothelin; ET-1; receptor; antagonist.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Ac-D-Trp"
XX
PN WO9414843-A1.
XX
PD 07-JUL-1994.
XX
PF 17-DEC-1993; 93WO-US012377.
XX
PR 21-DEC-1992; 92US-00995480.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Cody WL, Depue P, Doherty AM, He JX, Taylor MD;
XX WPI; 1994-234617/28.
DR
XX New hexa:peptide derivs. inhibiting endothelin - for treatment of e.g.
PT renal failure, hypertension, asthma, restenosis, angina, cancer etc.
XX
PS Claim 5; Page 119; 146pp; English.
XX
CC Novel antagonists of endothelin are claimed which are C-terminal
CC hexapeptides and analogs of ET-1. The first (N-terminal) amino acid of
CC the new peptides has D-configuration. The peptides are claimed
CC generically. The present peptide is a specifically claimed example of the
CC generic compounds. The peptides are useful for treating hypertension,
CC metabolic and endocrine disorders, congestive heart failure, myocardial
CC infarction, endotoxic shock, subarachnoid haemorrhage, arrhythmia,
CC asthma, acute and chronic renal failure, preeclampsia, diabetes,
CC neurological disorders, pulmonary hypertension, ischaemic disease,
CC ischaemic bowel disease, gastric mucosal damage, Raynaud's disease,
CC restenosis, percutaneous transluminal coronary angioplasty, angina and
CC cancer. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 5 AA;

Query Match 53.7%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLT I W 7
| | | |
Db 1 WLD I W 5

RESULT 8
AAW56531
ID AAW56531 standard; peptide; 5 AA.
XX

AC AAW56531;
XX
DT 06-AUG-1998 (first entry)
XX
DE Antigenic HIV-1 peptide used in diagnostic test device of invention.
XX
KW HIV-1; antigen; test device; detection; HIV infection; antibody;
KW whole blood; hormone; vitamin; microbial pathogen; drug.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
PN WO9813519-A1.
XX
PD 02-APR-1998.
XX
PF 25-SEP-1997; 97WO-US017129.
XX
PR 25-SEP-1996; 96US-0026681P.
PR 18-AUG-1997; 97US-00912580.
XX
PA (UVHE-) UNIVERSAL HEALTHWATCH INC.
XX
PI Childs MA, Bernstein D;
XX
DR WPI; 1998-230723/20.
XX
PT Diagnostic test device - provides homogeneous fluid flow and increased
PT chemical resistance, especially for detecting antibodies to human
PT immunodeficiency virus.
XX
PS Claim 39; Page 36; 50pp; English.
XX
CC AAW56525-36 represent antigenic Human immunodeficiency virus type 1 (HIV-
CC 1) peptides used in the test device of the invention. This test device
CC comprises, in a housing, an absorbent pad, a reagent layer containing
CC immobilised test antigens and a filter. The housing has an opening,
CC adjacent to the filter, for applying an aqueous sample, and the filter is
CC held in contact with the reagent layer by a sleeve. The filter protrudes
CC from the sleeve such that it exerts a greater pressure on the reagent
CC layer than does the sleeve. The device is specifically used to detect HIV
CC infection from presence of specific antibodies in whole blood, but many
CC other analytes can also be detected, e.g. amino acids, nucleic acid,
CC hormones, vitamins, microbial pathogens and drugs (therapeutic or
CC illicit)
XX
SQ Sequence 5 AA;
Query Match 53.7%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 LTIWG 8
DB 1 LTVWG 5
RESULT 9
ADJ25834
ID ADJ25834 standard; peptide; 7 AA.
XX
AC ADJ25834;
XX
DT 20-MAY-2004 (first entry)
XX
DE Tyrosine tRNA synthetase binding peptide group 2 motif.
XX
KW ligand identification; peptide library;
KW complementary combinatorial library; tyrosine tRNA synthetase.
XX
OS Synthetic.
XX
PN US6617114-B1.

XX 09-SEP-2003.
XX
PF 30-APR-1998; 98US-00069827.
XX
PR 31-OCT-1996; 96US-00740671.
PR 31-OCT-1997; 97WO-US019638.
PR 31-MAR-1998; 98US-00050359.
XX
PA (KARO-) KARO BIO AB.
XX
PI Fowlkes DM, Kay BK, Frelinger JA, Hyde-Deruysscher RP;
XX
DR WPI; 2004-068186/07.
XX
PT Identification of ligand that can mediate biological activity of target
PT protein, comprises screening first combinatorial library having first
PT member ligands for binding to target protein to identify target-binding
PT ligand(s).
XX
PS Example 5; SEQ ID NO 94; 98pp; English.
XX
CC The invention relates to a method of identifying a ligand that can
CC mediate the biological activity of target protein via inhibition of the
CC binding of target protein to a binding partner ligand comprising
CC screening first combinatorial library having first member ligands for
CC binding to target protein to identify target-binding ligand(s). The
CC method is useful for identifying ligands that can mediate the biological
CC activity of target proteins via inhibition of the binding of target
CC protein to a binding partner ligand. The invention does not require that
CC the natural binding partner be used as reagent. The need for the natural
CC binding partner is obviated with the use of complementary combinatorial
CC libraries. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 7 AA;
Query Match 53.7%; Score 29; DB 8; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 YWLTIWG 8
DB 1 YWWPDWG 7
RESULT 10
ABP22594
ID ABP22594 standard; peptide; 8 AA.
XX
AC ABP22594;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A11 motif env peptide #317.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX
XX WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PT
XX
XX Claim 32; Page 332; 448pp; English.
PS
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8
||:|
DB 2 LTVWG 6

RESULT 11
ABP14287
ID ABP14287 standard; peptide; 8 AA.
XX
AC ABP14287;
XX

DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX

DE HIV A03 super motif env peptide #27.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX

OS Human immunodeficiency virus 1.

XX WO200124810-A1.

PN 12-APR-2001.

PD 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

PR (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.
DR
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
PT
XX
XX Claim 32; Page 161; 448pp; English.
PS
XX

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8
||:|
DB 2 LTVWG 6

RESULT 12
ABP18686
ID ABP18686 standard; peptide; 8 AA.
XX
AC ABP18686;
XX

DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX

DE HIV B62 super motif env peptide #261.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX

OS Human immunodeficiency virus 1.

XX WO200124810-A1.

PN 12-APR-2001.

PD 05-OCT-2000; 2000WO-US027766.

XX 05-OCT-1999; 99US-00412863.

PR (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;

XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 252; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8
Db ||:|
3 LTVWG 7

RESULT 13
ABP20292
ID ABP20292 standard; peptide; 8 AA.
XX
AC ABP20292;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif env peptide #496.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 285; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 53.7%; Score 29; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8
Db ||:|
2 LTVWG 6

RESULT 14
ABP19992
ID ABP19992 standard; peptide; 8 AA.
XX
AC ABP19992;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif env peptide #196.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 279; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines. An

CC additional advantage of an group-based vaccine approach is the ability to

CC combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 8 AA;

Query Match 53.7%; Score 29; DB 4; Length 8;

Best Local Similarity 80.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8

Db ||:||

2 LTVWG 6

RESULT 15

ABP12050

ID ABP12050 standard; peptide; 8 AA.

XX

AC ABP12050;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV A02 super motif env peptide #107.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 116; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines. An

CC additional advantage of an group-based vaccine approach is the ability to

CC combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 8 AA;

Query Match 53.7%; Score 29; DB 4; Length 8;

Best Local Similarity 80.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIWG 8

Db ||:||

3 LTVWG 7

Search completed: January 3, 2005, 12:27:56

Job time : 150 secs

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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:23:00 ; Search time 37 Seconds
(without alignments)
14.339 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywlting 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 73656

Minimum DB seq length: 0
MaximumDBSeqLength: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match	Length	DB ID	Description
1	29	53.7	7	4	US-09-069-827A-94	Sequence 94, Appl
2	28	51.9	8	3	US-09-315-304B-1649	Sequence 1649, Ap
3	27.5	50.9	6	1	US-08-191-571-12	Sequence 12, Appl
4	27.5	50.9	6	5	PCT-US95-00296-12	Sequence 12, Appl
5	27	50.0	8	3	US-08-586-670A-17	Sequence 17, Appl
6	27	50.0	8	3	US-09-082-279B-1495	Sequence 1495, Ap
7	27	50.0	8	4	US-09-834-784-1495	Sequence 1495, Ap
8	27	50.0	8	4	US-09-350-641C-1650	Sequence 1650, Ap
9	26	48.1	5	1	US-08-353-400-27	Sequence 27, Appl
10	26	48.1	6	1	US-08-415-099A-3	Sequence 3, Appli
11	26	48.1	8	1	US-08-415-099A-4	Sequence 4, Appli
12	26	48.1	8	3	US-08-467-472C-5	Sequence 5, Appli
13	26	48.1	8	3	US-08-467-472C-6	Sequence 6, Appli
14	26	48.1	8	3	US-09-082-279B-1500	Sequence 1500, Ap
15	26	48.1	8	3	US-09-384-061-5	Sequence 5, Appli
16	26	48.1	8	3	US-09-384-061-6	Sequence 6, Appli
17	26	48.1	8	4	US-09-834-784-1500	Sequence 1500, Ap
18	26	48.1	8	4	US-08-632-444B-9	Sequence 9, Appli
19	26	48.1	8	4	US-09-350-641C-1655	Sequence 1655, Ap
20	26	48.1	8	4	US-09-852-870A-5	Sequence 5, Appli
21	25.5	47.2	8	1	US-08-191-571-21	Sequence 21, Appl
22	25.5	47.2	8	5	PCT-US95-00296-21	Sequence 21, Appl
23	25	46.3	5	4	US-09-155-106-1	Sequence 1, Appli
24	25	46.3	6	2	US-08-660-747-56	Sequence 56, Appl
25	25	46.3	8	4	US-09-125-641-1	Sequence 1, Appli
26	25	46.3	8	4	US-09-125-641-2	Sequence 2, Appli
27	24.5	45.4	8	3	US-08-481-968A-19	Sequence 19, Appl

28	24.5	45.4	8	3	US-08-154-712B-19	Sequence 19, Appl
29	24.5	45.4	8	4	US-09-947-925A-19	Sequence 19, Appl
30	24	44.4	5	4	US-08-753-750B-38	Sequence 38, Appl
31	24	44.4	5	6	5185431-15	Patent No. 5185431
32	24	44.4	6	1	US-07-718-577-6	Sequence 6, Appli
33	24	44.4	6	2	US-08-660-747-60	Sequence 60, Appl
34	24	44.4	7	3	US-09-082-279B-653	Sequence 653, App
35	24	44.4	7	3	US-09-315-304B-653	Sequence 653, App
36	24	44.4	7	3	US-09-315-304B-1579	Sequence 1579, Ap
37	24	44.4	7	4	US-09-388-788-2	Sequence 2, Appli
38	24	44.4	7	4	US-09-350-325-39	Sequence 39, Appl
39	24	44.4	7	4	US-09-834-784-653	Sequence 653, App
40	24	44.4	7	4	US-09-515-965A-653	Sequence 653, App
41	24	44.4	7	4	US-09-350-641C-653	Sequence 653, App
42	24	44.4	7	4	US-09-350-641C-1579	Sequence 1579, Ap
43	24	44.4	7	4	US-09-563-222C-53	Sequence 53, Appl
44	24	44.4	7	4	US-09-350-841A-653	Sequence 653, App
45	24	44.4	8	1	US-08-073-028-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-09-069-827A-94
; Sequence 94, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M
; KAY, Brian K
; FRELINGER, Jeffrey A
; HYDE-DERUYSCHE, Robin P
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
; COMPLEMENTARY COMBINATORIAL LIBRARIES
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:

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US-09-069-827A-94
;
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-191-571-12
;
; Query Match 50.9%; Score 27.5; DB 1; Length 6;
; Best Local Similarity 71.4%; Pred. No. 3.8e+05;
; Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YWLTWIG 8
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Db 1 YWLR-WG 6

RESULT 2
US-09-315-304B-1649
; Sequence 1649, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1649
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-315-304B-1649

Query Match 51.9%; Score 28; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLTWIG 8
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Db 1 WNSLWG 6

RESULT 3
US-08-191-571-12
; Sequence 12, Application US/08191571
; Patent No. 5521156
; GENERAL INFORMATION:
; APPLICANT: Owen, Thomas J.
; APPLICANT: Kudlacz, Elizabeth M
; APPLICANT: Buck, Stephen H
; APPLICANT: Harbeson, Scott L
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: P. O. Box 156300 2110 E. Galbraith Rd.
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/191,571
; FILING DATE: 03-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:

Query Match 50.9%; Score 27.5; DB 5; Length 6;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YWLTWIG 8
   ||| ||
Db 1 YWLR-WG 6

RESULT 5
US-09-069-827A-94
;
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-191-571-12
;
; Query Match 50.9%; Score 27.5; DB 1; Length 6;
; Best Local Similarity 71.4%; Pred. No. 3.8e+05;
; Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YWLTWIG 8
   ||| ||
Db 1 YWLR-WG 6

RESULT 4
PCT-US95-00296-12
; Sequence 12, Application PC/TUS9500296
; GENERAL INFORMATION:
; APPLICANT: Merrell Dow Pharmaceuticals Inc.
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marion Merrell Dow Inc.
; STREET: 2110 East Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45215-6300
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00296
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Boudreaux, William R
; REGISTRATION NUMBER: 35,796
; REFERENCE/DOCKET NUMBER: M01718A WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 513-948-6566
; TELEFAX: 513-948-7961 or 4681
; TELEX: 214320
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
PCT-US95-00296-12
;
; Query Match 50.9%; Score 27.5; DB 5; Length 6;
; Best Local Similarity 71.4%; Pred. No. 3.8e+05;
; Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 YWLTWIG 8
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Db 1 YWLR-WG 6

RESULT 5
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US-08-586-670A-17
; Sequence 17, Application US/08586670A
; Patent No. 6241965
; GENERAL INFORMATION:
; APPLICANT: McBride, William
; APPLICANT: Dean, Richard T.
; TITLE OF INVENTION: Somatostatin Derivatives
; TITLE OF INVENTION: And their Radiolabeled Products
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/586,670A
; FILING DATE: 22-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6241965nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,385-DD
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..2
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "Phe is in the D conformation and is
; OTHER INFORMATION: /note= "Phe is in the D conformation and is
; OTHER INFORMATION: linked to DTPA;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa
; OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the
; OTHER INFORMATION: D conformation;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7..8
; OTHER INFORMATION: /label= Variant residues
; OTHER INFORMATION: /note= "The carboxyl group of the C-terminal
; OTHER INFORMATION: Thr is reduced to an alcohol;
US-08-586-670A-17
Query Match 50.0%; Score 27; DB 3; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GYWLT 5
Db 2 GYWKT 6
RESULT 6
US-09-082-279B-1495
; Sequence 1495, Application US/09082279B
; Patent No. 6258782

US-08-586-670A-17
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1495
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-082-279B-1495
Query Match 50.0%; Score 27; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 WLTIWG 8
Db 1 WDSLWG 6
RESULT 7
US-09-834-784-1495
; Sequence 1495, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1495
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-09-834-784-1495
Query Match 50.0%; Score 27; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 WLTIWG 8
Db 1 WDSLWG 6
RESULT 8
US-09-350-641C-1650
; Sequence 1650, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; CURRENT FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1650
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
;
US-09-350-641C-1650

Query Match 50.0%; Score 27; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTWIG 8
| :|||
Db 1 WDSLWG 6

RESULT 9
US-08-353-400-27
; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-353-400-27

Query Match 48.1%; Score 26; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWL 4
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Db 1 GYWI 4

RESULT 10
US-08-415-099A-3
; Sequence 3, Application US/08415099A
; Patent No. 5789384
; GENERAL INFORMATION:
; APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.
; TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Ther

;
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cytoven
; STREET: .10230 N.E. Points Drive, Suite 530
; CITY: Kirkland
; STATE: Washington
; COUNTRY: USA
; ZIP: 98033
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.25 inch, 1.44Mb storage
; COMPUTER: IBM PC/486 Compatible
; OPERATING SYSTEM: MS-DOS 5.01
; SOFTWARE: Word for Windows 6.0-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,099A
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,386
; FILING DATE: 06-JUL-1994
; APPLICATION NUMBER: 08/026,341
; FILING DATE: March 4, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundemo, John, S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: 15548-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-889-5804(direct)
; TELEFAX: 1-206-822-3644
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
;
US-08-415-099A-3

Query Match 48.1%; Score 26; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTW 7
| :||
Db 2 WTW 6

RESULT 11
US-08-415-099A-4
; Sequence 4, Application US/08415099A
; Patent No. 5789384
; GENERAL INFORMATION:
; APPLICANT: Khavinson, V.Kh., Sery, S.V. and Morozov, V.G.
; TITLE OF INVENTION: "Pharmaceutical Dipeptide Compositions and Methods of Use Ther
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cytoven
; STREET: .10230 N.E. Points Drive, Suite 530
; CITY: Kirkland
; STATE: Washington
; COUNTRY: USA
; ZIP: 98033
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.25 inch, 1.44Mb storage
; COMPUTER: IBM PC/486 Compatible
; OPERATING SYSTEM: MS-DOS 5.01
; SOFTWARE: Word for Windows 6.0-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,099A
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/271,386
FILING DATE: 06-JUL-1994
APPLICATION NUMBER: 08/026,341
FILING DATE: March 4, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Sundemo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: 15548-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-889-5804(direct)
TELEFAX: 1-206-822-3644
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
US-0415-099A-4

Query Match 48.1%; Score 26; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLTW 7
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Db 2 WTW 6

RESULT 12
US-08-467-472C-5
Sequence 5, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:

DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-5

Query Match 48.1%; Score 26; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 WLTW 7
|: ||
Db 3 FWKTSW 8

RESULT 13
US-08-467-472C-6
; Sequence 6, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:

; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
; US-08-467-472C-6
; Query Match 48.1%; Score 26; DB 3; Length 8;
; Best Local Similarity 50.0%; Pred. No. 3.8e+05;
; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 YWLTIW 7
; :| | |
Db 3 FWKTSW 8
RESULT 14
US-09-082-279B-1500
; Sequence 1500, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1500
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
; US-09-082-279B-1500
; Query Match 48.1%; Score 26; DB 3; Length 8;
; Best Local Similarity 60.0%; Pred. No. 3.8e+05;
; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 WLTIW 7
; :| | |
Db 1 WASIW 5

RESULT 15
US-09-384-061-5
; Sequence 5, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:

; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
; US-09-384-061-5
Query Match 48.1%; Score 26; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 YWLTIW 7
Db 3 FWKTSW 8
Search completed: January 3, 2005, 12:32:37
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:31:17 ; Search time 140 Seconds
(without alignments)
20.556 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywltiwg 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 83711

Minimum DB seq length: 0
Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	61.1	7	13	US-10-046-922-67
2	33	61.1	8	13	US-10-046-922-68
3	27	50.0	8	14	US-10-351-641-1650
4	26	48.1	7	9	US-09-884-767A-38
5	26	48.1	7	16	US-10-433-452A-3
6	26	48.1	8	9	US-09-852-870A-5
7	26	48.1	8	14	US-10-351-641-1655
8	26	48.1	8	15	US-10-196-937A-9
9	26	48.1	8	16	US-10-457-780-38
10	25.5	47.2	8	15	US-10-367-580-227
11	25.5	47.2	8	15	US-10-367-593-227
12	25.5	47.2	8	15	US-10-367-594-227
13	25.5	47.2	8	15	US-10-367-654-227

14	25.5	47.2	8	15	US-10-367-658-227	Sequence 227, App
15	25.5	47.2	8	15	US-10-367-668-227	Sequence 227, App
16	25.5	47.2	8	16	US-10-367-674-227	Sequence 227, App
17	25	46.3	5	10	US-09-155-106-1	Sequence 1, Appli
18	25	46.3	7	14	US-10-190-082-65	Sequence 65, Appli
19	25	46.3	7	14	US-10-190-082-487	Sequence 487, App
20	25	46.3	7	17	US-10-858-271-10	Sequence 10, Appl
21	25	46.3	8	14	US-10-190-082-489	Sequence 489, App
22	25	46.3	8	14	US-10-050-902-179	Sequence 179, App
23	25	46.3	8	14	US-10-050-902-180	Sequence 180, App
24	25	46.3	8	14	US-10-050-898-179	Sequence 179, App
25	25	46.3	8	14	US-10-050-898-180	Sequence 180, App
26	25	46.3	8	14	US-10-082-014-279	Sequence 279, App
27	25	46.3	8	14	US-10-372-076-133	Sequence 133, App
28	25	46.3	8	15	US-10-149-138-35	Sequence 35, Appl
29	25	46.3	8	15	US-10-149-138-1999	Sequence 1999, Ap
30	25	46.3	8	15	US-10-617-876-31	Sequence 31, Appl
31	25	46.3	8	15	US-10-617-876-32	Sequence 32, Appl
32	25	46.3	8	16	US-10-149-138-35	Sequence 35, Appl
33	25	46.3	8	16	US-10-149-138-1999	Sequence 1999, Ap
34	25	46.3	8	16	US-10-677-074-133	Sequence 133, App
35	24.5	45.4	6	17	US-10-477-307-5	Sequence 5, Appli
36	24.5	45.4	8	9	US-09-947-925A-19	Sequence 19, Appl
37	24	44.4	4	16	US-10-386-575-12	Sequence 12, Appl
38	24	44.4	5	15	US-10-436-549-496	Sequence 496, App
39	24	44.4	5	15	US-10-436-549-525	Sequence 525, App
40	24	44.4	5	16	US-10-712-425-496	Sequence 496, App
41	24	44.4	5	16	US-10-712-425-525	Sequence 525, App
42	24	44.4	6	14	US-10-414-524-34	Sequence 34, Appl
43	24	44.4	6	14	US-10-407-079-65	Sequence 65, Appl
44	24	44.4	6	16	US-10-346-737A-45	Sequence 45, Appl
45	24	44.4	7	10	US-09-563-222-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-10-046-922-67
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046.922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-046-922-67

Query Match 61.1%; Score 33; DB 13; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
|||
Db 1 GYWXXW 7

RESULT 2
US-10-046-922-68
; Sequence 68, Application US/10046922

; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68

Query Match 61.1%; Score 33; DB 13; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWLTIW 7
| | | |
Db 1 GYWXXW 7

RESULT 3
US-10-351-641-1650
; Sequence 1650, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1650
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-10-351-641-1650

Query Match 50.0%; Score 27; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WLTIWG 8
| : | |
Db 1 WDSLWG 6

RESULT 4
US-09-884-767A-38

; Sequence 38, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-38

Query Match 48.1%; Score 26; DB 9; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWL 4
| | | |
Db 1 GYWI 4

RESULT 5
US-10-433-452A-3
; Sequence 3, Application US/10433452A
; Publication No. US20040101905A1
; GENERAL INFORMATION:
; APPLICANT: Brekke, Ole Henrik
; APPLICANT: Lauvrak, Vigdis
; APPLICANT: Sandlie, Inger
; TITLE OF INVENTION: Hybrid Antibodies
; FILE REFERENCE: DEH-0014
; CURRENT APPLICATION NUMBER: US/10/433,452A
; CURRENT FILING DATE: 2003-11-24
; PRIOR APPLICATION NUMBER: GB 0029407.4
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fc effector peptide
; NAME/KEY: VARIANT
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is R or a large hydrophobic amino acid, e.g. phenylalanine:
; OTHER INFORMATION: F, tyrosine: Y, or tryptophan: W
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (3)..(5)
; OTHER INFORMATION: Xaa is a less conserved or variable amino acid
US-10-433-452A-3

Query Match 48.1%; Score 26; DB 16; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WLTIWG 8
| | | |
Db 2 WXXXWG 7

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RESULT 6
US-09-852-870A-5
; Sequence 5, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-5

Query Match      48.1%; Score 26; DB 9; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 YWLTIW 7
      :|||
Db      3 FWKTSW 8

RESULT 7
US-10-351-641-1655
; Sequence 1655, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1655
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HIV-1
US-10-351-641-1655

Query Match      48.1%; Score 26; DB 14; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 WLTIW 7
      :|||
Db      1 WASIW 5

RESULT 8
US-10-196-937A-9
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; Sequence 9, Application US/10196937A
; Publication No. US20040024176A1
; GENERAL INFORMATION:
; APPLICANT: Ghadiri, Reza M.
; TITLE OF INVENTION: Cyclic Peptide Tube
; FILE REFERENCE: 397.2 Div 1/SCR 2381
; CURRENT APPLICATION NUMBER: US/10/196,937A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 08/632,444
; PRIOR FILING DATE: 1996-04-15
; PRIOR APPLICATION NUMBER: 08/320,922
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 08/138,502
; PRIOR FILING DATE: 1993-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Length: 8 amino acids
; OTHER INFORMATION: Type: amino acids
; OTHER INFORMATION: Topology: Circular
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 2
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 4
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 8
; OTHER INFORMATION: D-Leu or the D-isomer of the amino acid leucine
US-10-196-937A-9

Query Match      48.1%; Score 26; DB 15; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 WLTIW 7
      :|||
Db      1 WLWLW 5

RESULT 9
US-10-457-780-38
; Sequence 38, Application US/10457780
; Publication No. US20040137426A1
; GENERAL INFORMATION:
; APPLICANT: SERRES, Pierre-Francois
; APPLICANT: MOSCA, Joseph
; TITLE OF INVENTION: GP41 PEPTIDES AND METHODS BASED THEREON FOR INHIBITING HIV FUSION
; TITLE OF INVENTION: TO TARGET CELLS
; FILE REFERENCE: 118761
; CURRENT APPLICATION NUMBER: US/10/457,780
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/446,268
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/413,919
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/386,754
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 8
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: r-W8F
US-10-457-780-38

Query Match      48.1%; Score 26; DB 16; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 WLTIW 7
      ||:|
Db      4 WLSAW 8

RESULT 10
US-10-367-580-227
; Sequence 227, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-227

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWVVT-W 6

RESULT 11
US-10-367-593-227
; Sequence 227, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWVVT-W 6

RESULT 12
US-10-367-594-227
; Sequence 227, Application US/10367594
; Publication No. US20040071722A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461041
; CURRENT APPLICATION NUMBER: US/10/367,594
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/680,806
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-594-227

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWVVT-W 6

RESULT 13
US-10-367-594-227
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US-10-367-654-227
; Sequence 227, Application US/10367654
; Publication No. US20040071723A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461032
; CURRENT APPLICATION NUMBER: US/10/367,654
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/171,734
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/636,295
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-654-227

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWWVT-W 6

RESULT 14
US-10-367-658-227
; Sequence 227, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-227

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWWVT-W 6

RESULT 14
US-10-367-658-227
; Sequence 227, Application US/10367658
; Publication No. US20040071724A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461051
; CURRENT APPLICATION NUMBER: US/10/367,658
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,529
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
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; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-658-227

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWWVT-W 6

RESULT 15
US-10-367-668-227
; Sequence 227, Application US/10367668
; Publication No. US20040071725A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 227
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-227

Query Match      47.2%; Score 25.5; DB 15; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      1 GYWLTIW 7
      |:|:|
Db      1 GWWVT-W 6

Search completed: January 3, 2005, 12:43:11
Job time : 140 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:22:35 ; Search time 38 Seconds
(without alignments)
20.256 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywlting 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0
Maximum DB seq length: 8
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	22	40.7	7	2 PT0586	T-cell receptor be
2	20	37.0	5	2 JH0253	gut pentapeptide -
3	18	33.3	8	2 JS0315	leucokinin V - Mad
4	17	31.5	4	2 B53284	T-cell receptor be
5	17	31.5	6	2 PT0629	T-cell receptor be
6	17	31.5	6	2 PT0637	T-cell receptor be
7	17	31.5	6	2 A61068	locustakinin - mig
8	17	31.5	7	2 PT0628	T-cell receptor be
9	17	31.5	7	2 PT0642	T-cell receptor be
10	17	31.5	7	2 PT0722	T-cell receptor be
11	17	31.5	7	2 PT0728	T-cell receptor be
12	17	31.5	7	2 PX0008	glucuronosyltransf
13	17	31.5	7	2 B48394	major fat-globule
14	17	31.5	7	2 PD0029	pev-kinin 1 - pena
15	17	31.5	7	2 S57274	triacylglycerol li
16	17	31.5	7	2 S33244	neuromodulatory pe
17	17	31.5	7	2 S33245	neuromodulatory pe
18	17	31.5	7	2 S33246	neuromodulatory pe
19	17	31.5	8	2 PT0724	T-cell receptor be
20	17	31.5	8	2 JS0316	leucokinin VI - Ma
21	17	31.5	8	2 JS0317	leucokinin VII - M
22	17	31.5	8	2 JS0318	leucokinin VIII -
23	17	31.5	8	2 A31570	angiotensin-conver
24	16	29.6	7	2 S09652	hypothetical prote
25	15	27.8	6	2 PT0532	T-cell receptor be
26	15	27.8	6	2 F41946	T-cell receptor ga
27	15	27.8	7	4 A58725	virotaxin - destro
28	15	27.8	8	2 PH1618	Ig H chain V-D-J r
29	15	27.8	8	2 A59495	Vesicle associated

30	15	27.8	8	2 T13818	cytochrome oxidase
31	14	25.9	6	2 A31263	dihydrofolate redu
32	14	25.9	6	2 B35640	cerebellar degener
33	14	25.9	6	2 PT0519	T-cell receptor be
34	14	25.9	7	2 S21230	dermorphin (Trp-4,
35	14	25.9	7	2 PH1602	Ig H chain V-D-J r
36	14	25.9	7	2 S33567	tubulin beta-3 cha
37	13	24.1	4	2 S09478	globulin IV alpha
38	13	24.1	5	2 A32516	cholecystokinin-5
39	13	24.1	6	2 B34835	dnaA protein - Pse
40	13	24.1	6	2 B31263	dihydrofolate redu
41	13	24.1	6	2 A61411	ameletin - rat
42	13	24.1	7	1 A61324	dermorphin - Rohde
43	13	24.1	7	2 A60139	fatty-acid synthas
44	13	24.1	7	2 S71870	glutathione transf
45	13	24.1	7	2 S36662	dermorphin (Lys-7)

ALIGNMENTS

RESULT 1

PT0586
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0586
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor

Query Match 40.7%; Score 22; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 T1WG 8

Db 3 SIWG 6

RESULT 2

JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UES>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric, and of the circular muscle of the gastro-intestinal junction.

Query Match 37.0%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3

Db 1 GFW 3

RESULT 3
JS0315
leucokinin V - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0315
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic
A;Reference number: JS0315
A;Accession: JS0315
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19987
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.3%; Score 18; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GYWLTIWG 8
| : ||
Db 1 GSGFSSWG 8

RESULT 4
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: B53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germline diversity and j
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: B53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <HAR>
A;Cross-references: GB:S60737; NID:G233916; PIDN:AAB19518.1; PID:G233918
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 2 WG 3

RESULT 5
PT0629
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0629; PT0528
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0629
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
A;Accession: PT0528
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FE2>

A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 5 WG 6

RESULT 6
PT0637
T-cell receptor beta chain V-D-J region (111-1K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0637
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0637
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 5 WG 6

RESULT 7
A61068
locustakinin - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61068
R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.
Regul. Pept. 37, 49-57, 1992
A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, pri
A;Reference number: A61068; MUID:92262851; PMID:1585017
A;Accession: A61068
A;Molecule type: protein
A;Residues: 1-6 <SCH>
A;Cross-references: UNIPROT:P41491
C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide
F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 31.5%; Score 17; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
||
Db 5 WG 6

RESULT 8
PT0628
T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0628
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0628

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 31.5%; Score 17; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

||

Db 6 WG 7

RESULT 9

PT0642

T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0642

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0642

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

31.5%; Score 17; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

||

Db 5 WG 6

RESULT 10

PT0722

T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0722

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0722

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

31.5%; Score 17; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

||

Db 6 WG 7

RESULT 11

PT0728

T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0728

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0728

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-7 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match

31.5%; Score 17; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

||

Db 5 WG 6

RESULT 12

PX0008

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N;Alternate names: UDP-glucuronyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997

C;Accession: PX0008

R;Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver m

A;Reference number: PX0008; MUID:89197852; PMID:3149280

A;Accession: PX0008

A;Molecule type: protein

A;Residues: 1-7 <YOK>

C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match

31.5%; Score 17; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LTIW 7

| : |

Db 3 LLVW 6

RESULT 13

B48394

major fat-globule membrane protein GP 55 - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C;Accession: B48394

R;Mather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

II-like sequences.

A;Reference number: A48394; MUID:93250576; PMID:8485470

A;Accession: B48394

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MAT>

A;Experimental source: milk

A;Note: sequence extracted from NCBI backbone (NCBIP:131444)

Query Match

31.5%; Score 17; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8

||

Db 1 WG 2

RESULT 14
PD0029
pev-kinin 1 - penaeid shrimp (Penaeus vannamei) (fragment)
C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C;Accession: PD0029
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devreese, Biochem. Biophys. Res. Commun. 248, 406-411, 1998
A;Title: Identification of one tachykinin- and two kinin-related peptides in the brain of the shrimp Penaeus vannamei
A;Reference number: PD0027; MUID:98342103; PMID:9675150
A;Accession: PD0029
A;Molecule type: protein
A;Residues: 1-7 <NIE>
C;Comment: This peptide belongs to myotropic neuropeptides.

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8
||
Db 6 WG 7

RESULT 15
S57274
triacylglycerol lipase (EC 3.1.1.3) - Psychrobacter immobilis (fragment)
C;Species: Psychrobacter immobilis
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57274
R;Arpigny, J.L.; Feller, G.; Gerday, C. Biochim. Biophys. Acta 1263, 103, 1995
A;Title: Corrigendum to "Cloning, sequence and structural features of a lipase from the psychrophilic bacterium Psychrobacter immobilis"
A;Reference number: S57274; MUID:95359197; PMID:7632728
A;Accession: S57274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <ARP>
A;Cross-references: UNIPROT:Q02104; EMBL:X67712
C;Keywords: carboxylic ester hydrolase

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8
||
Db 1 WG 2

Search completed: January 3, 2005, 12:31:54
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 3, 2005, 12:14:40 ; Search time 189 Seconds
(without alignments)
24.354 Million cell updates/sec

Title: SEQ32
Perfect score: 54
Sequence: 1 gywlting 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 835

Minimum DB seq length: 0
Maximum-DB-seq-length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	48.1	8	2	Q70Y57 fuerstia af
2	26	48.1	8	2	CAD45547 fuerstia
3	21	38.9	8	2	AAB33374 homo sapi
4	20	37.0	7	2	Q8JE81 human immun
5	19	35.2	5	1	UF01_MOUSE mus musculu
6	18	33.3	8	1	LCK5_LEUMA leucophaea
7	18	33.3	8	1	PK4_PERAM periplaneta
8	18	33.3	8	2	Q62721 rattus norv
9	17	31.5	6	1	LOK1_LOCMI locusta mig
10	17	31.5	7	1	WWA1_ACHFU achatina fu
11	17	31.5	7	1	WWA2_ACHFU achatina fu
12	17	31.5	7	1	WWA3_ACHFU achatina fu
13	17	31.5	7	2	O49223 glycine max
14	17	31.5	8	1	AC1_THUAL thunnus alb
15	17	31.5	8	1	LCK1_LEUMA leucophaea
16	17	31.5	8	1	LCK2_LEUMA leucophaea
17	17	31.5	8	1	LCK3_LEUMA leucophaea
18	17	31.5	8	1	LCK4_LEUMA leucophaea
19	17	31.5	8	1	LCK6_LEUMA leucophaea
20	17	31.5	8	1	LCK7_LEUMA leucophaea
21	17	31.5	8	1	LCK8_LEUMA leucophaea
22	17	31.5	8	1	PK1_PERAM periplaneta
23	17	31.5	8	1	PK2_PERAM periplaneta
24	17	31.5	8	1	PK3_PERAM periplaneta
25	17	31.5	8	1	PK5_PERAM periplaneta
26	17	31.5	8	1	RT34_BOVIN bos taurus
27	17	31.5	8	2	Q70Y84 plectranthu
28	17	31.5	8	2	Q7GEM6 branchiosto
29	17	31.5	8	2	Q6ZZ01 silene con
30	17	31.5	8	2	Q6ZZ02 lychnis cor
31	17	31.5	8	2	CAD45500 plectrant

32	17	31.5	8	2	CAG24877	Cag24877 lychnis c
33	17	31.5	8	2	CAG24879	Cag24879 silene co
34	16	29.6	6	1	EI01_LITRU	P82096 litoria rub
35	16	29.6	7	2	Q9BRY4	Q9bry4 homo sapien
36	16	29.6	8	2	O85406	O85406 coxiella bu
37	15	27.8	4	1	OCP3_OCTMI	P58649 octopus min
38	15	27.8	8	1	VAM6_MOUSE	P83853 mus musculu
39	15	27.8	8	2	Q7I5L5	Q7i5l5 varanus dum
40	15	27.8	8	2	Q94V88	Q94v88 varanus tri
41	15	27.8	8	2	Q94V91	Q94v91 varanus tim
42	15	27.8	8	2	Q94VA7	Q94va7 varanus sal
43	15	27.8	8	2	Q94VB2	Q94vb2 varanus sal
44	15	27.8	8	2	Q94VB5	Q94vb5 varanus sal
45	15	27.8	8	2	Q94VC1	Q94vc1 varanus rud

ALIGNMENTS

RESULT 1

Q70Y57	Q70Y57	PRELIMINARY;	PRT;	8 AA.
AC	Q70Y57;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Ribosomal protein (Fragment).			
GN	Name=rp816;			
OS	Fuerstia africana.			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.			
OX	NCBI_TaxID=204226;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15019625;			
RA	Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,			
RA	Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;			
RT	"Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)			
RT	based on three plastid DNA regions.";			
RL	Mol. Phylogenet. Evol. 31:277-299(2004).			
DR	EMBL; AJ505427; CAD45547.1; -.			
KW	GO; GO:0003735; F:structural constituent of ribosome; IEA.			
FT	Ribosomal protein.			
FT	NON_TER 1 1			
FT	NON_TER 8 8			
SQ	SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;			

Query Match 48.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	5	TIWG 8
Db	2	TIWG 5

RESULT 2

CAD45547	CAD45547	PRELIMINARY;	PRT;	8 AA.
ID	CAD45547;			
AC	CAD45547;			
DT	14-MAR-2004 (TrEMBLrel. 27, Created)			
DT	14-MAR-2004 (TrEMBLrel. 27, Last sequence update)			
DT	14-MAR-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Ribosomal protein (Fragment).			
GN	RP816.			
OS	Fuerstia africana.			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Lamiids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fuerstia.			
OX	NCBI_TaxID=204226;			


```

RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Graver R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RA "Phylogeny and evolution of basilids and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 48.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TIWG 8
Db ||||
2 TIWG 5

RESULT 3
AAB33374
ID AAB33374 PRELIMINARY; PRT; 8 AA.
AC AAB33374;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Collagen alpha 5(IV) chain (Fragment).
GN COL4A5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95156893; PubMed=7853788;
RA Nakazato H., Hattori S., Ushijima T., Matsuura T., Koitabashi Y.,
RA Takada T., Yoshiooka K., Endo F., Matsuda I.;
RT "Mutations in the COL4A5 gene in Alport syndrome: a possible mutation
RT in primordial germ cells.";
RL Kidney Int. 46:1307-1314(1994).
DR EMBL; S75903; AAB33374.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 933 MW; 7370437735BAB378 CRC64;

Query Match 38.9%; Score 21; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WLTIW 7
Db |::|
2 WDSLW 6

RESULT 4
Q8JE81
ID Q8JE81 PRELIMINARY; PRT; 7 AA.
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
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RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAX32344.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTIW 7
Db ::|
3 ITLW 6

RESULT 5
UF01_MOUSE
ID UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=75231108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins using
RT preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON_TER 5
FT NON_TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 35.2%; Score 19; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 WLTIW 7
Db |::|
1 WIGRW 5

RESULT 6
LCK5_LEUMA
ID LCK5_LEUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=87052651; PubMed=2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinins V and VI:
RT myotropic peptides of Leucophaea maderae.";
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
```

```
CC      activity of cockroach protodeum (hindgut).
CC      -1- SUBCELLULAR LOCATION: Secreted.
DR      PIR; JS0315; JS0315.
KW      Amidation; Direct protein sequencing; Neuropeptide.
FT      MOD RES      8      Glycine amide.
SQ      SEQUENCE      8 AA; 784 MW; 736365A5B9C865B8 CRC64;

Query Match      33.3%; Score 18; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches      3; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

QY      1 GYWLTIWG 8
      | : ||
Db      1 GSGFSSWG 8

RESULT 7
PK4_PERAM
ID PK4_PERAM STANDARD; PRT; 8 AA.
AC P82688;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Kinin-4 (Pea-K-4).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=98010462; PubMed=9350979;
RA Predel R., Kellner R., Rapus J., Penzlin H., Gade G.;
RT "Isolation and structural elucidation of eight kinins from the
RT retrocerebral complex of the American cockroach, Periplaneta
RT americana.";
RL Regul. Pept. 71:199-205(1997).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=838.15; METHOD=Electrospray; RANGE=1-8;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the kinin family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES      8      Glycine amide.
SQ SEQUENCE      8 AA; 839 MW; 736365A5B9D6DDDB CRC64;

Query Match      33.3%; Score 18; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.8e+06;
Matches      3; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

QY      1 GYWLTIWG 8
      | : ||
Db      1 GAQFSSWG 8

RESULT 8
Q62721
ID Q62721 PRELIMINARY; PRT; 8 AA.
AC Q62721;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Prohibitin (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher;
RX MEDLINE=95331633; PubMed=7607556;

RA      Altus M.S., Wood C.M., Stewart D.A., Roskams A.I., Friedman V.,
RA      Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,
RA      McClung J.K.;
RT      "Regions of evolutionary conservation between the rat and human
RT      prohibitin-encoding genes.";
RL      Gene 158:291-294(1995).
DR      EMBL; U17178; AAA86692.1; -.
FT      NON_TER      8
SQ      SEQUENCE      8 AA; 1150 MW; EFD3237B05A41376 CRC64;

Query Match      33.3%; Score 18; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.8e+06;
Matches      2; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY      3 WLTIW 7
      | : |
Db      2 WRSEW 6

RESULT 9
LOK1_LOCMI
ID LOK1_LOCMI STANDARD; PRT; 6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT isolation, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -1- FUNCTION: Myotropic peptide. May be important in the stimulation
CC of ion transport and inhibition of diuretic activity in Malpighian
CC tubules.
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; A61068; A61068.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES      6      Glycine amide.
SQ SEQUENCE      6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match      31.5%; Score 17; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches      2; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      7 WG 8
      | |
Db      5 WG 6

RESULT 10
WWA1_ACHFU
ID WWA1_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Wwamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
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RC  TISSUE=Ganglion; PubMed=8495720;
RX  MEDLINE=93265912;
RA  Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT  "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL  ganglia of the African giant snail, Achatina fulica.";
CC  FEBS Lett. 323:104-108(1993).
CC  -!- FUNCTION: Exhibits modulatory effects on the peripheral nervous
CC  system. Inhibits activity on a central neuron.
DR  PIR; S33245; S33245.
KW  Amidation; Direct protein sequencing; Neuropeptide.
FT  MOD RES 7 Tryptophan amide.
SQ  SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTIW 7
Db 4 MSVW 7

RESULT 11
WWA2 ACHFV
ID _WWA2_ACHFV STANDARD; PRT; 7 AA.
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-2.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion; PubMed=8495720;
RX MEDLINE=93265912;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RL ganglia of the African giant snail, Achatina fulica.";
DR FEBS Lett. 323:104-108(1993).
DR PIR; S33246; S33246.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 Tryptophan amide.
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTIW 7
Db 4 MSVW 7

RESULT 12
WWA3 ACHFV
ID _WWA3_ACHFV STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion; PubMed=8495720;
RX MEDLINE=93265912;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
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RT  "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT  ganglia of the African giant snail, Achatina fulica.";
RL  FEBS Lett. 323:104-108(1993).
RL  PIR; S33244; S33244.
KW  Amidation; Direct protein sequencing; Neuropeptide.
FT  MOD RES 7 Tryptophan amide.
SQ  SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LTIW 7
Db 4 MSVW 7

RESULT 13
O49223
ID O49223 PRELIMINARY; PRT; 7 AA.
AC O49223;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HMG-1-like protein (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RX MEDLINE=91367679; PubMed=1891369;
RA Laux T., Goldberg R.B.;
RT "A plant DNA binding protein shares highly conserved sequence motifs
RT with HMG-box proteins.";
RL Nucleic Acids Res. 19:4769-4769(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RA Mahalingam R., Knap H.T.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF047050; AAC03556.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 31.5%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WG 8
Db 2 WG 3

RESULT 14
ACI_THUAL
ID _ACI_THUAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
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RX MEDLINE=88326322; PubMed=3415688;
RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
CC -!- FUNCTION: Inhibits angiotensin-converting enzyme.
DR PIR; A31570; A31570.
KW Direct protein sequencing; Metalloprotease inhibitor.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 31.5%; Score 17; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8
Db ||
6 WG 7

RESULT 15
LCK1_LEUMA
ID LCK1 LEUMA STANDARD; PRT; 8 AA.
AC P21140;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides from
Leucophaea maderae: members of a new family of Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211(1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
activity of cockroach protodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 8 8 Glycine amide.
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;

Query Match 31.5%; Score 17; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 WG 8
Db ||
7 WG 8

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